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INTERNATIONAL APPLICATION PUBLISHED UNDER THE PATENT COOPERATION TREATY (PCT)

(51) International Patent Classification 6 :
C12N 15/51, C07K 14/48, G01N 33/576, A61K 39/29, C12Q 1/68, 1/70

A2

(11) International Publication Number: WO 95/01442

(43) International Publication Date: 12 January 1995 (12.01.95)

(21) International Application Number: PCT/US94/07320

(22) International Filing Date: 28 June 1994 (28.06.94)

(30) Priority Data:
08/086,428 29 June 1993 (29.06.93) US

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(81) Designated States: AU, CA, JP, European patent (AT, BE, CH, DE, DK, ES, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE).

Published
Without international search report and to be republished upon receipt of that report.

(54) Title: NUCLEOTIDE AND AMINO ACID SEQUENCES OF THE ENVELOPE 1 GENE OF 51 HEPATITIS C VIRUS ISOLATES AND THE USE OF REAGENTS DERIVED THEREFROM AS DIAGNOSTIC REAGENTS AND VACCINES

(57) Abstract

The nucleotide and deduced amino acid sequences of 51 cDNAs are disclosed where each cDNA encodes the envelope 1 gene of an isolate of hepatitis C virus (HCV). The invention relates to the oligonucleotides, peptides and recombinant envelope 1 proteins derived from these sequences and their use in diagnostic methods and vaccines.

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Title of the Invention

NUCLEOTIDE AND AMINO ACID SEQUENCES OF THE ENVELOPE 1 GENE OF 51 HEPATITIS C VIRUS ISOLATES AND THE USE OF REAGENTS DERIVED THEREFROM AS DIAGNOSTIC REAGENTS AND VACCINES

Field Of Invention

The present invention is in the field of hepatitis virology. The invention relates to the complete nucleotide and deduced amino acid sequences of the envelope 1 (E1) gene of 51 hepatitis C virus (HCV) isolates from around the world and the grouping of these isolates into twelve distinct HCV genotypes. More specifically, this invention relates to oligonucleotides, peptides and recombinant proteins derived from the envelope 1 gene sequences of the 51 isolates of hepatitis C virus and to diagnostic methods and vaccines which employ these reagents.

Background Of Invention

Hepatitis C, originally called non-A, non-B hepatitis, was first described in 1975 as a disease serologically distinct from hepatitis A and hepatitis B (Feinstone, S.M. et al. (1975) N. Engl. J. Med. 292:767-770). Although hepatitis C was (and is) the leading type of transfusion-associated hepatitis as well as an important part of community-acquired hepatitis, little progress was made in understanding the disease until the recent identification of hepatitis C virus (HCV) as the causative agent of hepatitis C via the cloning and sequencing of the HCV genome (Choo, A.L. et al. (1989) Science 288:359-362). The sequence information generated by this study resulted in the characterization of HCV as a small, enveloped, positive-stranded RNA virus and led to the demonstration that HCV is a major cause of both acute and chronic hepatitis worldwide (Weiner, A.J. et al. (1990) Lancet

335:1-3). These observations, combined with studies showing that over 50% of acute cases of hepatitis C progress to chronicity with 20% of these resulting in cirrhosis and an undetermined proportion progressing to liver cancer, have led to tremendous efforts by investigators within the hepatitis C field to develop diagnostic assays and vaccines which can detect and prevent hepatitis C infection.

The cloning and sequencing of the HCV genome by Choo et al. (1989) has permitted the development of serologic tests which can detect HCV or antibody to HCV (Kuo, G. et al. (1989) Science 244:362-364). In addition, the work of Choo et al. has also allowed the development of methods for detecting HCV infection via amplification of HCV RNA sequences by reverse transcription and cDNA polymerase chain reaction (RT-PCR) using primers derived from the HCV genomic sequence (Weiner, A.J. et al.). However, although the development of these diagnostic methods has resulted in improved diagnosis of HCV infection, only approximately 60% of cases of hepatitis C are associated with a factor identified as contributing to transmission of HCV (Alter, M.J. et al. (1989) JAMA 262:1201-1205). This observation suggests that effective control of hepatitis C transmission is likely to occur only via universal pediatric vaccination as has been initiated recently for hepatitis B virus. Unfortunately, attempts to date to protect chimpanzees from hepatitis C infection via administration of recombinant vaccines have had only limited success. Moreover, the apparent genetic heterogeneity of HCV, as indicated by the recent assignment of all available HCV isolates to one of four genotypes, I-IV (Okamoto, H. et al. (1992) J. Gen. Virol; 73:673-679), presents additional hurdles which must be overcome in order to develop accurate and effective diagnostic assays and vaccines.

For example, one possible obstacle to the

development of effective hepatitis C vaccines would arise if the observed genetic heterogeneity of HCV reflects serologic heterogeneity. In such a case, the most genetically diverse strains of HCV may then represent different serotypes of HCV with the result being that infection with one strain may not protect against infection with another. Indeed, the inability of one strain to protect against infection with another strain was recently noted by both Farci et al. (Farci, P. et al. (1992) Science 258:135-140) and Prince et al. (Prince, A.M. et al. (1992) J. Infect. Dis. 165:438-443), each of whom presented evidence that while infection with one strain of HCV does modify the degree of the hepatitis C associated with the reinfection, it does not protect against reinfection with a closely related strain. The genetic heterogeneity among different HCV strains also increases the difficulty encountered in developing RT-PCR assays to detect HCV infection since such heterogeneity often results in false-negative results because of primer and template mismatch. In addition, currently used serologic tests for detection of HCV or for detection of antibody to HCV are not sufficiently well developed to detect all of the HCV genotypes which might exist in a given blood sample. Finally, in terms of choosing the proper treatment modality to combat hepatitis infection, the inability of presently available serologic assays to distinguish among the various genotypes of HCV represents a significant shortcoming in that recent reports suggest that an HCV-infected patient's response to therapy might be related to the genotype of the infectious virus (Yoshioka, K. et al. (1992) Hepatology 16:293-299; Kanai, K. et al. (1992) Lancet 339:1543; Lan, J.Y.N. et al. (1992) Hepatology 16:209A). Indeed, the data presented in the above studies suggest that the closely related genotypes I and II are less responsive to interferon therapy than are the closely related genotypes III and IV. Moreover, preliminary data by Pozzato et al.

(Pozzato, G. et al. (1991) Lancet 338:509) suggests that different genotypes may be associated with different types or degrees of clinical disease. Taken together, these studies suggest that before effective vaccines against HCV infection can be developed, and indeed, before more accurate and effective methods for diagnosis and treatment of HCV infection can be produced, one must obtain a greater knowledge about the genetic and serologic diversity of HCV isolates.

In a recent attempt to gain an understanding of the extent of genetic heterogeneity among HCV strains, Bukh et al. carried out a detailed analysis of HCV isolates via the use of PCR technology to amplify different regions of the HCV genome (Bukh, J. et al. (1992a) Proc. Natl. Acad. Sci. 89:187-191). Following PCR amplification, the 5'-noncoding (5' NC) portion of the genomes of various HCV isolates were sequenced and it was found that primer pairs designed from conserved regions of the 5' NC region of the HCV genome were more sensitive for detecting the presence of HCV than were primer pairs representing other portions of the genome (Bukh, J. et al. (1992b) Proc. Natl. Acad. Sci. U.S.A. 89:4942-4946). In addition, the authors noted that although many of the HCV isolates examined could be classified into the four genotypes described by Okamoto et al. (1992), other previously undescribed genotypes emerged based on genetic heterogeneity observed in the 5' NC region of the various isolates. One of the most prominent of these newly noted genotypes comprised a group of related viruses that contained the most genetically divergent 5' NC regions of those studied. This group of viruses, tentatively classified as a fifth genotype, are very similar to strains recently described by others (Cha, T.-A et al. (1992) Proc. Natl. Acad. Sci. U.S.A. 89:7144-7148; Chan, S-W. et al. (1992) J. Gen. Virol., 73:1131-1141 and Lee, C-H et al. (1992) J. Clin. Microbio. 30:1602-1604). In addition, at least four more putative genotypes were

identified thereby providing evidence that the genetic heterogeneity of HCV was more extensive than previously appreciated.

However, while the studies of Bukh et al. (1992a and b) provided new and useful information on the genetic heterogeneity of HCV, it is widely appreciated by those skilled in the art that the three structural genes of HCV, core (C), envelope (E1) and envelope 2/nonstructural 1 (E2/NS1) are the most important for the development of serologic diagnostics and vaccines since it is the product of these genes that constitutes the hepatitis C virion. Thus, a determination of the nucleotide sequence of one or all of the structural genes of a variety of HCV isolates would be useful in designing reagents for use in diagnostic assays and vaccines since a demonstration of genetic heterogeneity in a structural gene(s) of HCV isolates might suggest that some of the HCV genotypes represent distinct serotypes of HCV based upon the previously observed relationship between genetic heterogeneity and serologic heterogeneity among another group of single-stranded, positive-sense RNA viruses, the picornaviruses (Ruechert, R.R. "Picornaviridae and their replication", in Fields, B.N. et al., eds. Virology, New York: Raven Press, Ltd. (1990) 507-548).

Summary of Invention

The present invention relates to 51 cDNAs, each encoding the complete nucleotide sequence of the envelope 1 (E1) gene of an isolate of human hepatitis C virus (HCV).

The present invention also relates to the nucleic acid and deduced amino acid sequences of these E1 cDNAs.

It is an object of this invention to provide synthetic nucleic acid sequences capable of directing production of recombinant E1 proteins, as well as equivalent natural nucleic acid sequences. Such natural nucleic acid sequences may be isolated from a cDNA or

genomic library from which the gene capable of directing synthesis of the E1 proteins may be identified and isolated. For purposes of this application, nucleic acid sequence refers to RNA, DNA, cDNA or any synthetic variant thereof which encodes for peptides.

The invention also relates to the method of preparing recombinant E1 proteins derived from the E1 cDNA sequences by cloning the nucleic acid and inserting the cDNA into an expression vector and expressing the recombinant protein in a host cell.

The invention also relates to isolated and substantially purified recombinant E1 proteins and analogs thereof encoded by the E1 cDNAs.

The invention further relates to the use of recombinant E1 proteins as diagnostic agents and as vaccines.

The invention also relates to the use of single-stranded antisense poly- or oligonucleotides derived from the E1 cDNAs to inhibit the expression of the hepatitis C E1 gene.

The invention further relates to multiple computer-generated alignments of the nucleotide and deduced amino acid sequences of the 51 E1 cDNAs. These multiple sequence alignments serve to highlight regions of homology and non-homology between different sequences and hence, can be used by one skilled in the art to design peptides and oligonucleotides useful as reagents in diagnostic assays and vaccines.

The invention therefore also relates to purified and isolated peptides and analogs thereof derived from E1 cDNA sequences.

The invention further relates to the use of these peptides as diagnostic agents and vaccines.

The present invention also encompasses methods of detecting antibodies specific for hepatitis C virus in biological samples. The methods of detecting HCV or

antibodies to HCV disclosed in the present invention are useful for diagnosis of infection and disease caused by HCV and for monitoring the progression of such disease. Such methods are also useful for monitoring the efficacy of therapeutic agents during the course of treatment of HCV infection and disease in a mammal.

The invention also provides a kit for the detection of antibodies specific for HCV in a biological sample where said kit contains at least one purified and isolated peptide derived from the E1 cDNA sequences.

The invention further provides isolated and purified genotype-specific oligonucleotides and analogs thereof derived from E1 cDNA sequences.

The invention also relates to a method for detecting the presence of hepatitis C virus in a mammal, said method comprising analyzing the RNA of a mammal for the presence of hepatitis C virus. The invention further relates to a method for determining the genotype of hepatitis C virus present in a mammal. This method is useful in determining the proper course of treatment for an HCV-infected patient.

The invention also provides a diagnostic kit for the detection of hepatitis C virus in a biological sample. The kit comprises purified and isolated nucleic acid sequences useful as primers for reverse-transcription polymerase chain reaction (RT-PCR) analysis of RNA for the presence of hepatitis C virus.

The invention further provides a diagnostic kit for the determination of the genotype of a hepatitis C virus present in a mammal. The kit comprises purified and isolated nucleic acid sequences useful as primers for RT-PCR analysis of RNA for the presence of HCV in a biological sample and purified and isolated nucleic acid sequences useful as hybridization probes in determining the genotype of the HCV isolate detected in PCR.

This invention also relates to pharmaceutical

compositions for use in prevention or treatment of hepatitis C in a mammal.

Description of Figures

Figures 1 A-H show computer generated sequence alignments of the nucleotide sequences of the 51 HCV E1 cDNAs. The single letter abbreviations used for the nucleotides shown in Figures 1A-H are those standardly used in the art. Figure 1A shows the alignment of SEQ ID NOs:1-8 to produce a consensus sequence for genotype I/1a. Figure 1B shows the alignment of SEQ ID NOs:9-25 to produce a consensus sequence for genotype II/1b. Figure 1C shows the alignment of SEQ ID NOs:26-29 to produce a consensus sequence for genotype III/2a. Figure 1D shows the alignment of SEQ ID NOs:30-33 to produce a consensus sequence for genotype IV/2b. Figure 1E shows the alignment of SEQ ID NOs:35-39 to produce a consensus sequence for genotype V/3a. Figure 1F shows the computer alignment of SEQ ID NOs:42-43 to produce a consensus sequence for genotype 4C. Figure 1G shows the alignment of SEQ ID NOs:45-50 to produce a consensus sequence for genotype 5a. The nucleotides shown in capital letters in the consensus sequences of Figures 1A-G are those conserved within a genotype while nucleotides shown in lower case letters in the consensus sequences are those variable within a genotype. In addition, in Figures 1A-E and 1G, when the lower case letter is shown in a consensus sequence, the lower case letter represents the nucleotide found most frequently in the sequences aligned to produce the consensus sequence. In Figure 1E, the lower case letters shown in the consensus sequence are nucleotides in SEQ ID NO:42 which differ from nucleotides found in the same positions in SEQ ID NO:43. Finally, a hyphen at a nucleotide position in the consensus sequences in Figures 1A-6 indicates that two nucleotides were found in equal numbers at that position in the aligned sequences. In the

aligned sequences, nucleotides are shown in lower case letters if they differed from the nucleotides of both adjacent isolates. Figure 1H shows the alignment of the consensus sequences of Figures 1A-G with SEQ ID NO:34 (genotype 2c), SEQ ID NO:40 (genotype 4a), SEQ ID NO:41 (genotype 4b), SEQ ID NO:44 (genotype 4d) and SEQ ID NO:51 (genotype 6a) to produce a consensus sequence for all twelve genotypes. This consensus sequence is shown as the bottom line of Figure 1H where the nucleotides shown in capital letters are conserved among all genotypes and a blank space indicates that the nucleotide at that position is not conserved among all genotypes.

Figures 2A-H show computer alignments of the deduced amino acid sequences of the 51 HCV E1 cDNAs. The single letter abbreviations used for the amino acids shown in Figures 2A-H follow the conventional amino acid shorthand for the twenty naturally occurring amino acids. Figure 2A shows the alignment of SEQ ID NOs:52-59 to produce a consensus sequence for genotype I/1a. Figure 2B shows the alignment of SEQ ID NOs:60-76 to produce a consensus sequence for genotype II/1b. Figure 2C shows the alignment of SEQ ID NOs:77-80 to produce a consensus sequence for genotype III/2a. Figure 2D shows the alignment of SEQ ID NOs:81-84 to produce a consensus sequence for genotype IV/2b. Figure 2E shows the alignment of SEQ ID NOs:86-90 to produce a consensus sequence for genotype V/3a. Figure 2F shows the computer alignment of SEQ ID NOs:93-94 to produce a consensus sequence for genotype 4c. Figure 2G shows the alignment of SEQ ID NOs:96-101 to produce a consensus sequence for genotype 5a. The amino acids shown in capital letters in the consensus sequences of Figures 2A-G are those conserved within a genotype while amino acids shown in lower case letters in the consensus sequences are those variable within a genotype. In addition, in Figures 2A-E and 2G when the lower case letter is shown in a consensus sequence, the

letter represents the amino acid found most frequently in the sequences aligned to produce the consensus sequence. In Figure 2E, the lower case letters shown in the consensus sequence are amino acids in SEQ ID NO:93 which differ from amino acids found in the same positions in SEQ ID NO:94. Finally, a hyphen at an amino acid position in the consensus sequences of Figures 2A-G indicates that two amino acids were found in equal numbers at that position in the aligned sequences. In the aligned sequences, amino acids are shown in lower case letters if they differed from the amino acids of both adjacent isolates. Figure 2H shows the alignment of the consensus sequences of Figures 1A-G with SEQ ID NO:85 (genotype 2c), SEQ ID NO:91 (genotype 4a), SEQ ID NO:92 (genotype 4b), SEQ ID NO:95 (genotype 4d) and SEQ ID NO:102 (genotype 6a) to produce a consensus sequence for all twelve genotypes. This consensus sequence is shown as the bottom line of Figure 2H where the amino acids shown in capital letters are conserved among all genotypes and a blank space indicates that the amino acid at that position is not conserved among all genotypes.

Figure 3 shows multiple sequence alignment of the deduced amino acid sequence of the E1 gene of 51 HCV isolates collected worldwide. The consensus sequence of the E1 protein is shown in boldface (top). In the consensus sequence cysteine residues are highlighted with stars, potential N-linked glycosylation sites are underlined, and invariant amino acids are capitalized, whereas variable amino acids are shown in lower case letters. In the alignment, amino acids are shown in lower case letters if they differed from the amino acid of both adjacent isolates. Amino acid residues shown in bold print in the alignment represent residues which at that position in the amino acid sequence are genotype-specific. Amino acids that were invariant among all HCV isolates are shown as hyphens (-) in the alignment. Amino acid positions correspond to those of the HCV prototype sequence (HCV-1,

Choo, L. et al. (1991) Proc. Natl. Acad. Sci. USA 88:2451-2455) with the first amino acid of the E1 protein at position 192. The grouping of isolates into 12 genotypes (I/1a, II/1b, III/2a, IV/2b, V/3a, 2c, 4a, 4b, 4c, 4d, 5a and 6a) is indicated.

Figure 4 shows a dendrogram of the genetic relatedness of the twelve genotypes of HCV based on the percent amino acid identity of the E1 gene of the HCV genome. The twelve genotypes shown are designated as I/1a, II/1b, III/2a, IV/2b, V/3a, 2c, 4a, 4b, 4c, 4d, 5a and 6a. The shaded bars represent a range showing the maximum and minimum homology between the amino acid sequence of any one isolate of the genotype indicated and the amino acid sequence of any other isolate.

Figure 5 shows the distribution of the complete E1 gene sequence of 74 HCV isolates into the twelve HCV genotypes in the 12 countries studied. For 51 of these HCV isolates, including 8 isolates of genotype I/1a, 17 isolates of genotype II/1b and 26 isolates comprising the additional 10 genotypes, the complete E1 gene sequence was determined. In the remaining 23 isolates, all of genotypes I/1a and II/1b, the genotype assignment was based on only a partial E1 gene sequence. The partially sequenced isolates did not represent additional genotypes in any of the 12 countries. The number of isolates of a particular genotype is given in each of the 12 countries studied. For ease of viewing, those genotypes designated by two terms (e.g., I/1a) are indicated by the latter term (e.g. 1a). The designations used for each country are: Denmark (DK); Dominican Republic (DR); Germany (D); Hong Kong (HK); India (IND); Sardinia, Italy (S); Peru (P); South Africa (SA); Sweden (SW); Taiwan (T); United States (US); and Zaire (Z). National borders depicted in this figure represent those existing at the time of sampling.

Detailed Description Of Invention

The present invention relates to 51 cDNAs, each encoding the complete nucleotide sequence of the envelope 1 (E1) gene of an isolate of human hepatitis C virus (HCV). The cDNAs of the present invention were obtained as follows. Viral RNA was extracted from serum collected from humans infected with hepatitis C virus and the viral RNA was then reverse transcribed and amplified by polymerase chain reaction using primers deduced from the sequence of the HCV strain H-77 (Ogata, N. et al. (1991) Proc. Natl. Acad. Sci. U.S.A. 88:3392-3396). The amplified cDNA was then isolated by gel electrophoresis and sequenced.

The present invention further relates to the nucleotide sequences of the cDNAs encoding the E1 gene of the 51 HCV isolates. These nucleotide sequences are shown in the sequence listing as SEQ ID NO:1 through SEQ ID NO:51.

The abbreviations used for the nucleotides are those standardly used in the art.

The deduced amino acid sequence of each of SEQ ID NO:1 through SEQ ID NO:51 are presented in the sequence listing as SEQ ID NO:52 through SEQ ID NO:102 where the amino acid sequence in SEQ ID NO:52 is deduced from the nucleotide sequence shown in SEQ ID NO:1, the amino acid sequence shown in SEQ ID NO:53 is deduced from the nucleotide sequence shown in SEQ ID NO:2 and so on. The deduced amino acid sequence of each of SEQ ID Nos:52-102 starts at nucleotide 1 of the corresponding sequence shown in SEQ ID NOs:1-51 and extends 595 nucleotides.

The three letter abbreviations used in SEQ ID Nos:52-102 follow the conventional amino acid shorthand for the twenty naturally occurring amino acids.

Preferably, the E1 proteins or peptides of the present invention are substantially homologous to, and most preferably biologically equivalent to, the native HCV E1 proteins or peptides. By "biologically equivalent" as used

throughout the specification and claims, it is meant that the compositions are immunogenically equivalent to the native E1 proteins or peptides. The E1 proteins or peptides of the present invention may also stimulate the production of protective antibodies upon injection into a mammal that would serve to protect the mammal upon challenge with HCV. By "substantially homologous" as used throughout the ensuing specification and claims to describe E1 proteins and peptides, it is meant a degree of homology in the amino acid sequence to the native E1 proteins or peptides. Preferably the degree of homology is in excess of 90, preferably in excess of 95, with a particularly preferred group of proteins being in excess of 99 homologous with the native E1 proteins or peptides.

Variations are contemplated in the cDNA sequences shown in SEQ ID NO:1 through SEQ ID NO:51 which will result in a DNA sequence that is capable of directing production of analogs of the corresponding envelope 1 (E1) protein shown in SEQ ID NO:52 through SEQ ID NO:102. It should be noted that the DNA sequences set forth above represent a preferred embodiment of the present invention. Due to the degeneracy of the genetic code, it is to be understood that numerous choices of nucleotides may be made that will lead to a DNA sequence capable of directing production of the instant E1 protein or its analogs. As such, DNA sequences which are functionally equivalent to the sequence set forth above or which are functionally equivalent to sequences that would direct production of analogs of the E1 proteins produced pursuant to the amino acid sequences set forth above, are intended to be encompassed within the present invention.

The term analog as used throughout the specification or claims to describe the E1 proteins or peptides of the present invention, includes any protein or peptide having an amino acid residue sequence substantially identical to a sequence specifically shown herein in which

one or more residues have been conservatively substituted with a biologically equivalent residue. Examples of conservative substitutions include the substitution of one-polar (hydrophobic) residue such as isoleucine, valine, leucine or methionine for another, the substitution of one polar (hydrophilic) residue for another such as between arginine and lysine, between glutamine and asparagine, between glycine and serine, the substitution of one basic residue such as lysine, arginine or histidine for another, or the substitution of one acidic residue, such as aspartic acid or glutamic acid for another.

The phrase "conservative substitution" also includes the use of a chemically derivatized residue in place of a non-derivatized residue provided that the resulting protein or peptide is biologically equivalent to the native E1 protein or peptide.

"Chemical derivative" refers to an E1 protein or peptide having one or more residues chemically derivatized by reaction of a functional side group. Examples of such derivatized molecules, include but are not limited to, those molecules in which free amino groups have been derivatized to form amine hydrochlorides, p-toluene sulfonyl groups, carbobenzoxy groups, t-butyloxycarbonyl groups, chloracetyl groups or formyl groups. Free carboxyl groups may be derivatized to form salts, methyl and ethyl esters or other types of esters or hydrazides. Free hydroxyl groups may be derivatized to form O-acyl or O-alkyl derivatives. The imidazole nitrogen of histidine may be derivatized to form N-imbenzylhistidine. Also included as chemical derivatives are those proteins or peptides which contain one or more naturally-occurring amino acid derivatives of the twenty standard amino acids. For examples: 4-hydroxyproline may be substituted for proline; 5-hydroxylysine may be substituted for lysine; 3-methylhistidine may be substituted for histidine; homoserine may be substituted for serine; and ornithine may

be substituted for lysine. The E1 protein or peptide of the present invention also includes any protein or peptide having one or more additions and/or deletions or residues relative to the sequence of a peptide whose sequence is shown herein, so long as the peptide is biologically equivalent to the native E1 protein or peptide.

The present invention also includes a recombinant DNA method for the manufacture of HCV E1 proteins. In this method, natural or synthetic nucleic acid sequences may be used to direct the production of E1 proteins.

In one embodiment of the invention, the method comprises:

(a) preparation of a nucleic acid sequence capable of directing a host organism to produce HCV E1 protein;

(b) cloning the nucleic acid sequence into a vector capable of being transferred into and replicated in a host organism, such vector containing operational elements for the nucleic acid sequence;

(c) transferring the vector containing the nucleic acid and operational elements into a host organism capable of expressing the protein;

(d) culturing the host organism under conditions appropriate for amplification of the vector and expression of the protein; and

(e) harvesting the protein.

In another embodiment of the invention, the method for the recombinant DNA synthesis of an HCV E1 protein encoded by any one of the nucleic acid sequences shown in SEQ ID NOs:1-51 comprises:

(a) culturing a transformed or transfected host organism containing a nucleic acid sequence capable of directing the host organism to produce a protein, under conditions such that the protein is produced, said protein exhibiting substantial homology to a native E1 protein isolated from HCV having the amino acid sequence according

to any one of the amino acid sequences shown in SEQ ID NOs:52-102 or combinations thereof.

In one embodiment, the RNA sequence of an HCV isolate was isolated and cloned to cDNA as follows. Viral RNA is extracted from a biological sample collected from human subjects infected with hepatitis C and the viral RNA is then reverse transcribed and amplified by polymerase chain reaction using primers deduced from the sequence of HCV strain H-77 (Ogata et al. (1991)). Preferred primer sequences are shown as SEQ ID NOs:103-108 in the sequence listing. Once amplified, the PCR fragments are isolated by gel electrophoresis and sequenced.

The vectors contemplated for use in the present invention include any vectors into which a nucleic acid sequence as described above can be inserted, along with any preferred or required operational elements, and which vector can then be subsequently transferred into a host organism and replicated in such organisms. Preferred vectors are those whose restriction sites have been well documented and which contain the operational elements preferred or required for transcription of the nucleic acid sequence.

The "operational elements" as discussed herein include at least one promoter, at least one operator, at least one leader sequence, at least one terminator codon, and any other DNA sequences necessary or preferred for appropriate transcription and subsequent translation of the vector nucleic acid. In particular, it is contemplated that such vectors will contain at least one origin of replication recognized by the host organism along with at least one selectable markers and at least one promoter sequence capable of initiating transcription of the nucleic acid sequence.

In construction of the recombinant for expression cloning vector of the present invention, it should additionally be noted that multiple copies of the nucleic

acid sequence and its attendant operational elements may be inserted into each vector. In such an embodiment, the host organism would produce greater amounts per vector of the desired E1 protein. The number of multiple copies of the DNA sequence which may be inserted into the vector is limited only by the ability of the resultant vector due to its size, to be transferred into and replicated and transcribed in an appropriate host microorganism.

In another embodiment, restriction digest fragments containing a coding sequence for E1 proteins can be inserted into a suitable expression vector that functions in prokaryotic or eukaryotic cells. By suitable is meant that the vector is capable of carrying and expressing a complete nucleic acid sequence coding for E1 protein. Preferred expression vectors are those that function in a eukaryotic cell. Examples of such vectors include but are not limited to vaccinia virus vectors, adenovirus or herpes viruses. A preferred vector is the baculovirus transfer vector, pBlueBac.

In yet another embodiment, the selected recombinant expression vector may then be transfected into a suitable eukaryotic cell system for purposes of expressing the recombinant protein. Such eukaryotic cell systems include but are not limited to cell lines such as HeLa, MRC-5 or Cv-1. A preferred eukaryotic cell system is SF9 insect cells.

The expressed recombinant protein may be detected by methods known in the art including, but not limited to, Coomassie blue staining and Western blotting.

The present invention also relates to substantially purified and isolated recombinant E1 proteins. In one embodiment, the recombinant protein expressed by the SF9 cells can be obtained as a crude lysate or it can be purified by standard protein purification procedures known in the art which may include differential precipitation, molecular sieve chromatography,

ion-exchange chromatography, isoelectric focusing, gel electrophoresis and affinity and immunoaffinity chromatography. The recombinant protein may be purified by passage through a column containing a resin which has bound thereto antibodies specific for the open reading frame (ORF) protein.

The present invention further relates to the use of recombinant E1 proteins as diagnostic agents and vaccines. In one embodiment, the expressed recombinant proteins of this invention can be used in immunoassays for diagnosing or prognosing hepatitis C in a mammal. For the purposes of the present invention, "mammal" as used throughout the specification and claims, includes, but is not limited to humans, chimpanzees, other primates and the like. In a preferred embodiment, the immunoassay is useful in diagnosing hepatitis C infection in humans.

Immunoassays of the present invention may be a radioimmunoassay, Western blot assay, immunofluorescent assay, enzyme immunoassay, chemiluminescent assay, immunohistochemical assay and the like. Standard techniques known in the art for ELISA are described in Methods in Immunodiagnosis, 2nd Edition, Rose and Bigazzi, eds., John Wiley and Sons, 1980 and Campbell et al., Methods of Immunology, W.A. Benjamin, Inc., 1964, both of which are incorporated herein by reference. Such assays may be a direct, indirect, competitive, or noncompetitive immunoassay as described in the art (Oellerich, M. 1984. J. Clin. Chem. Clin. BioChem 22:895-904) Biological samples appropriate for such detection assays include, but are not limited to serum, liver, saliva, lymphocytes or other mononuclear cells.

In a preferred embodiment, test serum is reacted with a solid phase reagent having surface-bound recombinant HCV E1 protein as an antigen. The solid surface reagent can be prepared by known techniques for attaching protein to solid support material. These attachment methods

include non-specific adsorption of the protein to the support or covalent attachment of the protein to a reactive group on the support. After reaction of the antigen with anti-HCV antibody, unbound serum components are removed by washing and the antigen-antibody complex is reacted with a secondary antibody such as labelled anti-human antibody. The label may be an enzyme which is detected by incubating the solid support in the presence of a suitable fluorimetric or calorimetric reagent. Other detectable labels may also be used, such as radiolabels or colloidal gold, and the like.

The HCV E1 protein and analogs thereof may be prepared in the form of a kit, alone, or in combinations with other reagents such as secondary antibodies, for use in immunoassays.

In yet another embodiment the recombinant E1 proteins or analogs thereof can be used as a vaccine to protect mammals against challenge with Hepatitis C. The vaccine, which acts as an immunogen, may be a cell, cell lysate from cells transfected with a recombinant expression vector or a culture supernatant containing the expressed protein. Alternatively, the immunogen is a partially or substantially purified recombinant protein.

While it is possible for the immunogen to be administered in a pure or substantially pure form, it is preferable to present it as a pharmaceutical composition, formulation or preparation.

The formulations of the present invention, both for veterinary and for human use, comprise an immunogen as described above, together with one or more pharmaceutically acceptable carriers and optionally other therapeutic ingredients. The carrier(s) must be "acceptable" in the sense of being compatible with the other ingredients of the formulation and not deleterious to the recipient thereof. The formulations may conveniently be presented in unit dosage form and may be prepared by any method well-known in

the pharmaceutical art.

All methods include the step of bringing into association the active ingredient with the carrier which constitutes one or more accessory ingredients. In general, the formulations are prepared by uniformly and intimately bringing into association the active ingredient with liquid carriers or finely divided solid carriers or both, and then, if necessary, shaping the product into the desired formulation.

Formulations suitable for intravenous intramuscular, subcutaneous, or intraperitoneal administration conveniently comprise sterile aqueous solutions of the active ingredient with solutions which are preferably isotonic with the blood of the recipient. Such formulations may be conveniently prepared by dissolving the solid active ingredient in water containing physiologically compatible substances such as sodium chloride (e.g. 0.1-2.0m), glycine, and the like, and having a buffered pH compatible with physiological conditions to produce an aqueous solution, and rendering said solution sterile. These may be present in unit or multi-dose containers, for example, sealed ampoules or vials.

The formulations of the present invention may incorporate a stabilizer. Illustrative stabilizers are preferably incorporated in an amount of 0.11-10,000 parts by weight per part by weight of immunogens. If two or more stabilizers are to be used, their total amount is preferably within the range specified above. These stabilizers are used in aqueous solutions at the appropriate concentration and pH. The specific osmotic pressure of such aqueous solutions is generally in the range of 0.1-3.0 osmoles, preferably in the range of 0.8-1.2. The pH of the aqueous solution is adjusted to be within the range of 5.0-9.0, preferably within the range of 6-8. In formulating the immunogen of the present invention, anti-adsorption agent may be used.

Additional pharmaceutical methods may be employed to control the duration of action. Controlled release preparations may be achieved through the use of polymer to complex or adsorb the proteins or their derivatives. The controlled delivery may be exercised by selecting appropriate macromolecules (for example polyester, polyamino acids, polyvinyl pyrrolidone, ethylenevinylacetate, methylcellulose, carboxymethylcellulose, or protamine sulfate) and the concentration of macromolecules as well as the methods of incorporation in order to control release. Another possible method to control the duration of action by controlled-release preparations is to incorporate the proteins, protein analogs or their functional derivatives, into particles of a polymeric material such as polyesters, polyamino acids, hydrogels, poly(lactic acid) or ethylene vinylacetate copolymers. Alternatively, instead of incorporating these agents into polymeric particles, it is possible to entrap these materials in microcapsules prepared, for example, by coacervation techniques or by interfacial polymerization, for example, hydroxymethylcellulose or gelatin-microcapsules and poly (methylmethacylate) microcapsules, respectively, or in colloidal drug delivery systems, for example, liposomes, albumin microspheres, microemulsions, nanoparticles, and nanocapsules or in macroemulsions.

When oral preparations are desired, the compositions may be combined with typical carriers, such as lactose, sucrose, starch, talc, magnesium stearate, crystalline cellulose, methyl cellulose, carboxymethyl cellulose, glycerin, sodium alginate or gum arabic among others.

The proteins of the present invention may be supplied in the form of a kit, alone, or in the form of a pharmaceutical composition as described above.

Vaccination can be conducted by conventional

methods. For example, the immunogen or immunogens (i.e. the E1 protein may be administered alone or in combination with the E1 proteins derived from other isolates of HCV) can be used in a suitable diluent such as saline or water, or complete or incomplete adjuvants. Further, the immunogen(s) may or may not be bound to a carrier to make the protein(s) immunogenic. Examples of such carrier molecules include but are not limited to bovine serum albumin (BSA), keyhole limpet hemocyanin (KLH), tetanus toxoid, and the like. The immunogen(s) can be administered by any route appropriate for antibody production such as intravenous, intraperitoneal, intramuscular, subcutaneous, and the like. The immunogen(s) may be administered once or at periodic intervals until a significant titer of anti-HCV antibody is produced. The antibody may be detected in the serum using an immunoassay.

The administration of the immunogen(s) of the present invention may be for either a prophylactic or therapeutic purpose. When provided prophylactically, the immunogen(s) is provided in advance of any exposure to HCV or in advance of any symptom of any symptoms due to HCV infection. The prophylactic administration of the immunogen serves to prevent or attenuate any subsequent infection of HCV in a mammal. When provided therapeutically, the immunogen(s) is provided at (or shortly after) the onset of the infection or at the onset of any symptom of infection or disease caused by HCV. The therapeutic administration of the immunogen(s) serves to attenuate the infection or disease.

In addition to use as a vaccine, the compositions can be used to prepare antibodies to HCV E1 proteins. The antibodies can be used directly as antiviral agents. To prepare antibodies, a host animal is immunized using the E1 proteins native to the virus particle bound to a carrier as described above for vaccines. The host serum or plasma is collected following an appropriate time interval to provide

a composition comprising antibodies reactive with the E1 protein of the virus particle. The gamma globulin fraction or the IgG antibodies can be obtained, for example, by use of saturated ammonium sulfate or DEAE Sephadex, or other techniques known to those skilled in the art. The antibodies are substantially free of many of the adverse side effects which may be associated with other anti-viral agents such as drugs.

The antibody compositions can be made even more compatible with the host system by minimizing potential adverse immune system responses. This is accomplished by removing all or a portion of the Fc portion of a foreign species antibody or using an antibody of the same species as the host animal, for example, the use of antibodies from human/human hybridomas. Humanized antibodies (i.e., nonimmunogenic in a human) may be produced, for example, by replacing an immunogenic portion of an antibody with a corresponding, but nonimmunogenic portion (i.e., chimeric antibodies). Such chimeric antibodies may contain the reactive or antigen binding portion of an antibody from one species and the Fc portion of an antibody (nonimmunogenic) from a different species. Examples of chimeric antibodies, include but are not limited to, non-human mammal-human chimeras, rodent-human chimeras, murine-human and rat-human chimeras (Robinson et al., International Patent Application 184,187; Taniguchi M., European Patent Application 171,496; Morrison et al., European Patent Application 173,494; Neuberger et al., PCT Application WO 86/01533; Cabilly et al., 1987 Proc. Natl. Acad. Sci. USA 84:3439; Nishimura et al., 1987 Canc. Res. 47:999; Wood et al., 1985 Nature 314:446; Shaw et al., 1988 J. Natl. Cancer Inst. 80:15553, all incorporated herein by reference).

General reviews of "humanized" chimeric antibodies are provided by Morrison S., 1985 Science 229:1202 and by Oi et al., 1986 BioTechniques 4:214.

Suitable "humanized" antibodies can be

alternatively produced by CDR or CEA substitution (Jones et al., 1986 Nature 321:552; Verhoeyan et al., 1988 Science 239:1534; Biedleret al. 1988 J. Immunol. 141:4053, all incorporated herein by reference).

The antibodies or antigen binding fragments may also be produced by genetic engineering. The technology for expression of both heavy and light cain genes in E. coli is the subject of the PCT patent applications; publication number WO 901443, WO901443, and WO 9014424 and in Huse et al., 1989 Science 246:1275-1281.

The antibodies can also be used as a means of enhancing the immune response. The antibodies can be administered in amount similar to those used for other therapeutic administrations of antibody. For example, normal immune globulin is administered at 0.02-0.1 ml/lb body weight during the early incubation period of other viral diseases such as rabies, measles, and hepatitis B to interfere with viral entry into cells. Thus, antibodies reactive with the HCV E1 protein can be passively administered alone or in conjunction with another anti-viral agent to a host infected with an HCV to enhance the immune response and/or the effectiveness of an antiviral drug.

Alternatively, anti-HCV E1 antibodies can be induced by administered anti-idiotype antibodies as immunogens. Conveniently, a purified anti-HCV E1 antibody preparation prepared as described above is used to induce anti-idiotype antibody in a host animal, the composition is administered to the host animal in a suitable diluent. Following administration, usually repeated administration, the host produces anti-idiotype antibody. To eliminate an immunogenic response to the Fc region, antibodies produced by the same species as the host animal can be used or the Fc region of the administered antibodies can be removed. Following induction of anti-idiotype antibody in the host animal, serum or plasma is removed to provide an antibody

composition. The composition can be purified as described above for anti-HCV E1 antibodies, or by affinity chromatography using anti-HCV E1 antibodies bound to the affinity matrix. The anti-idiotype antibodies produced are similar in conformation to the authentic HCV E1 protein and may be used to prepare an HCV vaccine rather than using an HCV E1 protein.

When used as a means of inducing anti-HCV virus antibodies in an animal, the manner of injecting the antibody is the same as for vaccination purposes, namely intramuscularly, intraperitoneally, subcutaneously or the like in an effective concentration in a physiologically suitable diluent with or without adjuvant. One or more booster injections may be desirable.

The HCV E1 proteins of the invention are also intended for use in producing antiserum designed for pre- or post-exposure prophylaxis. Here an E1 protein, or mixture of E1 proteins is formulated with a suitable adjuvant and administered by injection to human volunteers, according to known methods for producing human antisera. Antibody response to the injected proteins is monitored, during a several-week period following immunization, by periodic serum sampling to detect the presence of anti-HCV E1 serum antibodies, using an immunoassay as described herein.

The antiserum from immunized individuals may be administered as a pre-exposure prophylactic measure for individuals who are at risk of contracting infection. The antiserum is also useful in treating an individual post-exposure, analogous to the use of high titer antiserum against hepatitis B virus for post-exposure prophylaxis.

For both <u>in vivo</u> use of antibodies to HCV virus-like particles and proteins and anti-idiotype antibodies and diagnostic use, it may be preferable to use monoclonal antibodies. Monoclonal anti-HCV E1 protein antibodies or anti-idiotype antibodies can be produced as follows. The

spleen or lymphocytes from an immunized animal are removed and immortalized or used to prepare hybridomas by methods known to those skilled in the art. (Goding, J.W. 1983. Monoclonal Antibodies: Principles and Practice, Pladermic Press, Inc., NY, NY, pp. 56-97). To produce a human-human hybridoma, a human lymphocyte donor is selected. A donor known to be infected with HCV (where infection has been shown for example by the presence of anti-virus antibodies in the blood or by virus culture) may serve as a suitable lymphocyte donor. Lymphocytes can be isolated from a peripheral blood sample or spleen cells may be used if the donor is subject to splenectomy. Epstein-Barr virus (EBV) can be used to immortalize human lymphocytes or a human fusion partner can be used to produce human-human hybridomas. Primary in vitro immunization with peptides can also be used in the generation of human monoclonal antibodies.

Antibodies secreted by the immortalized cells are screened to determine the clones that secrete antibodies of the desired specificity. For monoclonal anti-E1 antibodies, the antibodies must bind to HCV E1 protein. For monoclonal anti-idiotype antibodies, the antibodies must bind to anti-E1 protein antibodies. Cells producing antibodies of the desired specify are selected.

The present invention also relates to the use of single-stranded antisense poly- or oligonucleotides derived from nucleotide sequences substantially homologous to those shown in SEQ ID NOs:1-51 to inhibit the expression of hepatitis C E1 genes. By substantially homologous as used throughout the specification and claims to describe the nucleic acid sequences of the present invention, is meant a level of homology between the nucleic acid sequence and the SEQ ID NOs. referred to in that sentence. Preferably, the level of homology is in excess of 80%, more preferably in excess of 90%, with a preferred nucleic acid sequence being in excess of 95% homologous with the DNA sequence shown in

the indicated SEQ ID NO. These anti-sense poly- or oligonucleotides can be either DNA or RNA. The targeted sequence is typically messenger RNA and more preferably, a single sequence required for processing or translation of the RNA. The anti-sense poly- or oligonucleotides can be conjugated to a polycation such as polylysine as disclosed in Lemaitre, M. et al. ((1989) Proc. Natl. Acad. Sci. USA 84:648-652) and this conjugate can be administrated to a mammal in an amount sufficient to hybridize to and inhibit the function of the messenger RNA.

The present invention further relates to multiple computer-generated alignments of the nucleotide and deduced amino acid sequences shown in SEQ ID NOs:1-102. Computer analysis of the nucleotide sequences shown in SEQ ID NOs:1-51 and of the deduced amino acid sequences shown in SEQ ID NOs:52-102 can be carried out using commercially available computer programs known to one skilled in the art.

In one embodiment, computer analysis of SEQ ID NOs:1-51 by the program GENALIGN (Intelligenetics, Inc. Mountainview, CA) results in distribution of the 51 sequences into twelve genotypes based upon the degree of variation of the sequences. For the purposes of the present invention, the nucleotide sequence identity of E1 cDNAs of HCV isolates of the same genotype is in the range of about 85% to about 100% whereas the identity of E1 cDNA sequences of different genotypes is in the range of about 50% to about 80%.

The grouping of SEQ ID NOs:1-51 into twelve HCV genotypes is shown below.

SEQ ID NOs:	Genotypes
1-8	I/1a
9-25	II/1b
26-29	III/2a
30-33	IV/2b
34	2c
35-39	V/3a
40	4a
41	4b
42-43	4c
44	4d
45-50	5a
51	6a

For those genotypes containing more than one E1 nucleotide sequence, computer alignment of the constituent nucleotide sequences of the genotype was conducted using GENALIGN in order to produce a consensus sequence for each genotype. These alignments and their resultant consensus sequences are shown in Figures 1A-G for the seven genotypes (I/1a, II/1b, III/2a, IV/2b, V/3a, 4c and 5a) which comprise more than one nucleotide sequence. Further alignment of the consensus sequences of Figures 1A-G with SEQ ID NO:34 (genotype 2c), SEQ ID NO:40 (genotype 4a), SEQ ID NO:41 (genotype 4b), SEQ ID NO:44 (genotype 4d) and SEQ ID NO:51 (genotype 6a) produces a consensus sequence for all twelve genotypes as shown in Figure 1H. The multiple alignments of nucleotide sequences shown in Figures 1A-H serve to highlight regions of homology and non-homology between different sequences and hence, can be used by one skilled in the art to design oligonucleotides useful as reagents in diagnostic assays for HCV.

Examples of purified and isolated oligonucleotide sequences provided by the present invention are shown as SEQ ID NOs:109-135. The oligonucleotides shown in SEQ ID NOs:109-135 are useful as "genotype-specific" primers and probes since these oligonucleotides can hybridize specifically to the nucleotide sequence of the E1 gene of HCV isolates belonging to a single genotype. The genotype-specificity of the oligonucleotides shown in SEQ ID

NOs:109-135 is as follows: SEQ ID NOs:109-110 are specific for genotype I/1a; SEQ ID NOs:111-112 are specific for genotype II/1b; SEQ ID NOs:113-114 are specific for genotype III/2a; SEQ ID NOs:115-116 are specific for genotype IV/2b; SEQ ID NOs:117-119 are specific for genotype 2c; SEQ ID NOs:120-122 are specific for genotype V/3a; SEQ ID NOs:123-124 are specific for genotype 4a; SEQ ID NOs:125-125 are specific for genotype 4b; SEQ ID NOs:127-128 are specific for genotype 4c; SEQ ID NOs:129-130 are specific for genotype 4d; SEQ ID NOs:131-132 are specific for genotype 5a and SEQ ID NOs:133-135 are specific for genotype 6a.

The oligonucleotides of this invention can be synthesized using any of the known methods of oligonucleotide synthesis (e.g., the phosphodiester method of Agarwal et al. 1972, Agnew. Chem. Int. Ed. Engl. 11:451, the phosphotriester method of Hsiung et al. 1979, Nucleic Acids Res 6:1371, or the automated diethylphosphoramidite method of Baeucage et al. 1981, Tetrahedron Letters 22:1859-1862), or they can be isolated fragments of naturally occurring or cloned DNA. In addition, those skilled in the art would be aware that oligonucleotides can be synthesized by automated instruments sold by a variety of manufacturers or can be commercially custom ordered and prepared. In a preferred embodiment, SEQ ID NO:103 through SEQ ID NO:135, are synthetic oligonucleotides.

The present invention also relates to a method for detecting the presence of HCV in a mammal, said method comprising analyzing the RNA of a mammal for the presence of hepatitis C virus.

The RNA to be analyzed can be isolated from serum, liver, saliva, lymphocytes or other mononuclear cells as viral RNA, whole cell RNA or as poly(A)$^+$ RNA. Whole cell RNA can be isolated by methods known to those skilled in the art. Such methods include extraction of RNA by differential precipitation (Birnbiom, H.C. (1988)

Nucleic Acids Res., 16:1487-1497), extraction of RNA by organic solvents (Chomczynski, P. et al. (1987) Anal. Biochem., 162:156-159) and extraction of RNA with strong denaturants (Chirgwin, J.M. et al. (1979) Biochemistry, 18:5294-5299). Poly(A)$^+$ RNA can be selected from whole cell RNA by affinity chromatography on oligo-d(T) columns (Aviv, H. et al. (1972) Proc. Natl. Acad. Sci., 69:1408-1412). A preferred method of isolating RNA is extraction of viral RNA by the quanidium-phenol-chloroform method of Bukh et al. (1992a).

The methods for analyzing the RNA for the presence of HCV include Northern blotting (Alwine, J.C. et al. (1977) Proc. Natl. Acad. Sci., 74:5350-5354), dot and slot hybridization (Kafatos, F.C. et al. (1979) Nucleic Acids Res., 7:1541-1522), filter hybridization (Hollander, M.C. et al. (1990) Biotechniques; 9:174-179), RNase protection (Sambrook, J. et al. (1989) in "Molecular Cloning, A Laboratory Manual", Cold Spring Harbor Press, Plainview, NY) and reverse-transcription polymerase chain reaction (RT-PCR) (Watson, J.D. et al. (1992) in "Recombinant DNA" Second Edition, W.H. Freeman and Company, New York). A preferred method is RT-PCR. In this method, the RNA can be reverse transcribed to first strand cDNA using a primer or primers derived from the nucleotide sequences shown in SEQ ID NOs:1-51. A preferred primer for reverse transcription is that shown in SEQ ID NO:104. Once the cDNAs are synthesized, PCR amplification is carried out using pairs of primers designed to hybridize with sequences in the HCV E1 cDNA which are an appropriate distance apart (at least about 50 nucleotides) to permit amplification of the cDNA and subsequent detection of the amplification product. Each primer of a pair is a single-stranded oligonucleotide of about 20 to about 60 bases in length where one primer (the "upstream" primer) is complementary to the original RNA and the second primer (the "downstream" primer) is complementary to the first strand of cDNA

generated by reverse transcriptions of the RNA. The target sequence is generally about 100 to about 300 base pairs long but can be as large as 500-1500 base pairs. Optimization of the amplification reaction to obtain sufficiently specific hybridization to the E1 nucleotide sequence is well within the skill in the art and is preferably achieved by adjusting the annealing temperature.

In one embodiment, the primer pairs selected to amplify E1 cDNAs are universal primers. By "universal", as used to describe primers throughout the claims and specification, is meant those primer pairs which can amplify E1 gene fragments derived from an HCV isolate belonging to any one of the twelve genotypes of HCV described herein. Purified and isolated universal primers are used in Example 1 of the present invention and are shown as SEQ ID NOs:103-108 where SEQ ID NOs:103 and 104 represent one pair of primers, SEQ ID NOs:105 and 106 represent a second pair of primers and SEQ ID NOs:107-108 represent a third pair of primers.

In an alternative embodiment, primer pairs selected to amplify E1 cDNAs are genotype-specific primers. In the present invention, genotype-specific primer pairs can readily be derived from the following genotype-specific nucleotide domains: nucleotides 197-238 and 450-480 of the consensus sequence of genotype I/1a shown in Figure 1A; nucleotides 197-238 and 450-480 of the consensus sequence of genotype II/1b shown in Figure 1B; nucleotides 199-238 and 438-480 of the consensus sequence of genotype III/2a shown in Figure C; nucleotides 124-177 and 450-480 of the consensus sequence of genotype IV/2b shown in Figure 1D; nucleotides 124-177, 193-238 and 436-480 of SEQ ID NO:34 (genotype 2C); nucleotides 168-207, 294-339 and 406-480 of the consensus sequence of genotype V/3a shown in Figure 1E; nucleotides 145-183 and 439-480 of SEQ ID NO:40 (genotype 4a); nucleotides 168-207 and 432-480 of SEQ ID NO:41 (genotype 4b); nucleotides 130-183 and 450-480 of the

consensus sequence of genotype 4c shown in Figure 1F; nucleotides 130-183 and 450-480 of SEQ ID NO:44 (genotype 4d); nucleotides 166-208 and 437-480 of the consensus sequence of genotype 5a shown in Figure 1b and nucleotides 168-207, 216-252 and 429-480 of SEQ ID NO:51 (genotype 6a). One skilled in the art would readily appreciate that in a pair of genotype-specific primers, each primer is derived from different genotype-specific nucleotide domains indicated above for a given genotype. Also, as described earlier, it is understood by one skilled in the art that each pair of primers comprises one primer which is complementary to the original viral RNA and the other which is complementary to the first strand of cDNA generated by reverse transcription of the viral RNA. For example, in a pair of genotype-specific primers for genotype 4b, one primer would have a nucleotide sequence derived from region 168-207 of SEQ ID NO:40 and the other primer would have a nucleotide sequence which is the complement of region 432-480 of SEQ ID NO:40. One skilled in the art would readily recognize that such genotype specific domains would also be useful in designing oligonucleotides for use as genotype-specific hybridization probes. Indeed, the sequences of such genotype-specific hybridization probes are disclosed later in the specification.

The amplification products of PCR can be detected either directly or indirectly. In one embodiment, direct detection of the amplification products is carried out via labelling of primer pairs. Labels suitable for labelling the primers of the present invention are known to one skilled in the art and include radioactive labels, biotin, avidin, enzymes and fluorescent molecules. The derived labels can be incorporated into the primers prior to performing the amplification reaction. A preferred labelling procedure utilizes radiolabeled ATP and T4 polynucleotide kinase (Sambrook, J. et al. (1989) in "Molecular Cloning, A Laboratory Manual", Cold Spring

Harbor Press, Plainview, NY). Alternatively, the desired label can be incorporated into the primer extension products during the amplification reaction in the form of one or more labelled dNTPs. In the present invention, the labelled amplified PCR products can be detected by agarose gel electrophoresis followed by ethidum bromide staining and visualization under ultraviolet light or via direct sequencing of the PCR-products.

In yet another embodiment, unlabelled amplification products can be detected via hybridization with labelled nucleic acid probes radioactively labelled or, labelled with biotin, in methods known to one skilled in the art such as dot and slot blot hybridization (Kafatos, F.C. et al. (1979) or filter hybridization (Hollander, M.C. et al. (1990)).

In one embodiment, the nucleic acid sequences used as probes are selected from, and substantially homologous to, SEQ ID NOs:1-51. Such probes are useful as universal probes in that they can detect in PCR-amplification products of E1 cDNAs of an HCV isolate belonging to any of the twelve HCV genotypes disclosed herein. The size of these probes can range from about 200 to about 500 nucleotides.

In an alternative embodiment, the present invention relates to a method for determining the genotype of a hepatitis C virus present in a mammal where said method comprises:

(a) amplifying RNA of a mammal via RT-PCR to produce amplification products;

(b) contacting said products with at least one genotype-specific oligonucleotide; and

(c) detecting complexes of said products which bind to said oligonucleotide(s).

In this method, one embodiment of said amplification step is carried out using the universal primers (SEQ ID NO:103 through SEQ ID NO:108) as disclosed

above. In step (b) of this method, the nucleic acid sequences used as probes are substantially homologous to the sequences shown in SEQ ID NOs:109-135. The probes disclosed in SEQ ID NOs:109-135 are useful in specifically detecting PCR-amplification products of E1 cDNAs of HCV isolates belonging to one of the twelve HCV genotypes disclosed herein. In a preferred embodiment, probes having sequences substantially homologous to the sequences shown in SEQ ID NOs:109-135 are used alone or in combination with other probes specific to the same genotype.

For example, a probe having a sequence according to SEQ ID NO:109 can be used alone or in combination with a probe having a sequence according to SEQ ID NO:110. The probes derived from SEQ ID NOs:109-135 can range in size from about 30 to about 70 nucleotides and can be synthesized as described earlier.

The nucleic acid sequence used as a probe to detect PCR amplification products of the present invention can be labeled in single-stranded or double-stranded form. Labelling of the nucleic acid sequence can be carried out by techniques known to one skilled in the art. Such labelling techniques can include radiolabels and enzymes (Sambrook, J. et al. (1989) in "Molecular Cloning, A Laboratory Manual", Cold Spring Harbor Press, Plainview, New York). In addition, there are known non-radioactive techniques for signal amplification including methods for attaching chemical moieties to pyrimidine and purine rings (Dale, R.N.K. et al. (1973) Proc. Natl. Acad. Sci., 70:2238-2242; Heck, R.F. (1968) S. Am. Chem. Soc., 90:5518-5523), methods which allow detection by chemiluminescence (Barton, S.K. et al. (1992) J. Am. Chem. Soc., 114:8736-8740) and methods utilizing biotinylated nucleic acid probes (Johnson, T.K. et al. (1983) Anal. Biochem., 133:126-131; Erickson, P.F. et al. (1982) J. of Immunology Methods, 51:241-249; Matthaei, F.S. et al. (1986) Anal. Biochem., 157:123-128) and methods which allow detection by

fluorescence using commercially available products.

The present invention also relates to computer analysis of the amino acid sequences shown in SEQ ID NOs:52-102 by the program GENALIGN. This analysis groups the 51 amino acid sequences shown in SEQ ID NOs:52-102 into the twelve genotypes disclosed earlier in this application based upon the degree of variation of the amino acid sequences. For the purposes of the present invention, the amino acid sequence identity of E1 amino acid sequences of the same genotype ranges from about 85% to about 100% whereas the identity of E1 sequences of different genotypes ranges from about 45% to about 80%.

The grouping of SEQ ID NOs:52-102 into the twelve HCV genotypes is shown below:

SEQ ID NOs:	Genotypes
52-59	I/1a
60-76	II/1b
77-80	III/2a
81-84	IV/2b
85	2c
86-90	V/3a
91	4a
92	4b
93-94	4c
95	4d
96-101	5a
102	6a

For those genotypes containing more than one E1 amino acid sequence, computer alignment of the constituent sequences of each genotype was conducted using the computer program GENALIGN in order to produce a consensus sequence for each genotype. These alignments and their resultant consensus sequences are shown in Figures 2A-G for the seven genotypes (I/1a, II/1b, III/2a, IV/2b, V/3a, 4c and 5a) which comprise more than one sequence. Further alignment of the consensus sequences shown in Figures 2A-G with the amino acid sequences of SEQ ID NO:85 (genotype 2c); SEQ ID NO:91 (genotype 4a); SEQ ID NO:92 (genotype 4b); SEQ ID

NO:95 (genotype 4d) and SEQ ID NO:102 (genotype 6a) to produce a consensus amino acid sequence for all twelve genotypes is shown in Figure 2H. The multiple alignment of E1 amino acid sequences shown in Figures 2A-H serves to highlight regions of homology and non-homology between amino acid sequences and hence, these alignments can readily be used by one skilled in the art to derive peptides useful in assays and vaccines for the diagnosis and prevention of HCV infection. Examples of purified and isolated peptides are provided by the present invention are shown as SEQ ID NOs:136-159. These peptides are derived from two regions of the amino acid sequences shown in Figures 2A-H, amino acids 48-80 and amino acids 138-160. The peptides shown in SEQ ID NOs:136-159 are useful as genotype-specific diagnostic reagents since they are capable of detecting an immune response specific to HCV isolates belonging to a single genotype. The genotype-specificity of the peptides shown in SEQ ID NOs:136-159 are as follows: SEQ ID NOs:136 and 148 are specific for genotype IV/2b; SEQ ID NOs:137 and 149 are specific for genotype 2c; SEQ ID NOs:138 and 150 are specific for genotype III/2a; SEQ ID NOs:139 and 151 are specific for genotype V/a; SEQ ID NOs:140 and 152 are specific for genotype II/1b; SEQ ID NOs:141 and 153 are specific for genotype I/1a; SEQ ID NOs:142 and 154 are specific for genotype 4a; SEQ ID NOs:143 and 155 are specific for genotype 4c; SEQ ID NOs:144 and 156 are specific for genotype 4d; SEQ ID NOs:145 and 157 are specific for genotype 4b; SEQ ID NOs:146 and 158 are specific for genotype 5a and SEQ ID NOs:147 and 159 are specific for genotype 6a. In SEQ ID NO:136, Xaa at position 22 is a residue of Ala or Thr, Xaa at position 24 is a residue of Val or Ile, Xaa at position 26 is a residue of Val or Met; in SEQ ID NO:138, Xaa at position 5 is a Ser or Thr residue, Xaa at position 11 is an Arg or Gln residue, Xaa at position 12 is an Arg or Gln residue; in SEQ ID NO:139,

Xaa at position 3 is a Pro or Ser residue, Xaa at position 33 is a Leu or Met residue; in SEQ ID NO:140, Xaa at position 5 is a Thr or Ala residue, Xaa at position 13 is a Gly, Ala, Ser, Val or Thr residue, Xaa at position 14 is a Ser, Thr or Asn residue, Xaa at position 15 is a Val or Ile residue, Xaa at position 16 is a Pro or Ser residue, Xaa at position 18 is a Thr or Lys residue, Xaa at position 19 is a Thr or Ala residue, Xaa at position 22 is an Arg or His residue, Xaa at position 32 is an Ala, Val or Thr residue; in SEQ ID NO:141, Xaa at position 3 is an Ala or Pro residue, Xaa at position 4 is a Val or Met residue, Xaa at position 5 is a Thr or Ala residue, Xaa at position 17 is a Thr or Ala residue, Xaa at position 18 is a Thr or Ala residue, Xaa at position 23 is a His or Tyr residue; in SEQ ID NO:143, Xaa at position 10 is a Val or Ala residue, Xaa at position 11 is a Ser or Pro residue, Xaa at position 18 is an Asp or Glu residue Xaa at position 20 is a Leu or Ile residue; in SEQ ID NO:146, Xaa at position 3 is a Gln or His residue, Xaa at position 12 is an Asn, Ser or Thr residue, Xaa at position 13 is a Leu or Phe residue, Xaa at position 23 is an Ala or Val residue; in SEQ ID NO:148, Xaa at position 16 is a Val or Ala residue, Xaa at position 18 is a Glu or Gln residue; in SEQ ID NO:150, Xaa at position 2 is an Ala or Thr residue, Xaa at position 4 is a Met or Leu residue, Xaa at position 9 is an Ala or Val residue, Xaa at position 17 is an Ile or Leu residue, Xaa at position 20 is an Ile or Val residue, Xaa at position 21 is a Ser or Gly residue; in SEQ ID NO:151, Xaa at position 9 is a Val or Ile residue, Xaa at position 16 is a Leu or Val residue, Xaa at position 20 is an Ile or Leu residue; in SEQ ID NO:152, Xaa at position 2 is an Ala or Thr residue, Xaa at position 6 is a Val or Leu residue, Xaa at position 12 is an Ile or Leu residue, Xaa at position 16 is a Val or Ile residue, Xaa at position 17 is a Val, Leu or Met residue, Xaa at position 19 is a Met or Val residue, Xaa at position 21 is an Ala or Thr residue; in SEQ ID NO:153, Xaa

at position 2 is a Thr or Ala residue, Xaa at position 6 is a Val, Ile or Met residue, Xaa at position 12 is an Ile or Val residue, Xaa at position 16 is a Ile or Val residue; in SEQ ID NO:155, Xaa at position 5 is a Leu or Val residue, Xaa at position 21 is a Thr or Ala residue; in SEQ ID NO:158, Xaa at position 1 is a Thr or Ala residue, Xaa at position 5 is a Val or Leu residue, Xaa at position 9 is a Leu, Met or Val residue, Xaa at position 23 is a Gly or Ala residue.

Those skilled in the art would be aware that the peptides of the present invention or analogs thereof can be synthesized by automated instruments sold by a variety of manufacturers or can be commercially custom-ordered and prepared. The term analog has been described earlier in the specification and for purposes of describing the peptides of the present invention, analogs can further include branched or non-linear arrangements of the peptide sequences shown in SEQ ID NOs:136-159.

Alternatively, peptides can be expressed from nucleic acid sequences where such sequences can be DNA, cDNA, RNA or any variant thereof which is capable of directing protein synthesis. In one embodiment, restriction digest fragments containing a coding sequence for a peptide can be inserted into a suitable expression vector that functions in prokaryotic or eukaryotic cells. Such restriction digest fragments may be obtained from clones isolated from prokaryotic or eukaryotic sources which encode the peptide sequence.

Suitable expression vectors and methods of isolating clones encoding the peptide sequences of the present invention have previously been described.

The preferred size of the peptides of the present invention is from about 8 to about 100 amino acids in length.

The present invention further relates to the use of the peptides shown in SEQ ID NOs:136-159 in methods of

detecting antibodies specific for HCV in biological samples. In one embodiment, at least one peptide specific for a single genotype to be used in previously described immunoassays to detect antibodies specific for a single genotype of HCV. A preferred immunoassay is ELISA.

It is understood by one skilled in the art that the diagnostic assays described herein using genotype-specific oligonucleotides or genotype-specific peptides ca be useful in assisting one skilled in the art to choose a course of therapy for the HCV-infected individual.

In an alternative embodiment, a mixture of peptides can be used in an immunoassay to detect antibodies to any of the twelve genotypes of HCV. The mixture of peptides as disclosed herein, comprises at least one peptide selected from SEQ ID NOs:140-141 and 152-153; one peptide selected from SEQ ID NOs:136, 138, 148 and 150; one peptide selected from SEQ ID NOs:142-145 and 154-157; one peptide selected from SEQ ID NOs:146 and 158; one peptide selected from SEQ ID NOs:139 and 151; one peptide selected from SEQ ID NOs:138 and 150 and one peptide selected from SEQ ID NOs:140 and 159. In a preferred embodiment, the peptides of the present invention can be used in an ELISA assay as described previously for E1 proteins.

The peptides or analogs thereof may be prepared in the form of a kit, alone or in combinations with other reagents such as secondary antibodies, for use in immunoassay. In addition, since genotype-specific peptides shown in SEQ ID NOs:136-159 are derived from two variable regions in the E1 protein, amino acids 48-80 (SEQ ID NOs:136-147) and amino acids 138-160 (SEQ ID NOs:148-159), one skilled in the art would recognize that these peptides would be useful as vaccines against hepatitis C. In the present invention, a peptide from SEQ ID NOs:136-159 can be used alone or in combination with other peptides shown therein as immunogens in the vaccine. Formulations suitable for administering the peptide(s) of the present

invention, routes of administration, pharmaceutical compositions comprising the peptid s and so forth are the same as those previously described for recombinant E1 proteins. In addition, as described for E1 proteins, the peptide(s) can also be used to prepare antibodies to HCV-E1 protein.

The peptides of the present invention may also be supplied in the form of a kit, alone, or in the form of a pharmaceutical composition as described above for E1 proteins recombinant.

Any articles or patents referenced herein are incorporated by reference. The following examples illustrate various aspects of the invention but are in no way intended to limit the scope thereof.

MATERIALS

Serum used in these examples was obtained from 84 anti-HCV positive individuals that were previously found to be positive for HCV RNA in a cDNA PCR assay with primer set *a* from the 5' NC region of the HCV genome (Bukh, J. et al. (1992 (b)) Natl. Acad. Sci. USA 89:4942-4946). These samples were from 12 countries: Denmark (DK); Dominican Republic (DR); Germany (D); Hong Kong (HK); India (IND); Sardinia, Italy (S); Peru (P); South Africa (SA); Sweden (SW); Taiwan (T); United States (US); and Zaire (Z).

Example 1

Identification of the DNA Sequence of the E1 Gene of 51 Isolates of HCV via RT-PCR Analysis of Viral RNA Using Universal Primers

Viral RNA was extracted from 100 μl of serum by the guanidinium-phenol-chloroform method and the final RNA solution was divided into 10 equal aliquots and stored at -80°C as described (Bukh, et al. (1992 (a)). The sequences of the synthetic oligonucleotides used in the RT-PCR assay, deduced from the sequence of HCV strain H-77 (Ogata, N. et al. (1991) Proc. Natl. Acad. Sci. USA 88:3392-3396), are shown as SEQ ID NOs:103-108. One aliquot of the final RNA solution, equivalent to 10 μl of serum, was used for cDNA synthesis that was performed in a 20 μl reaction mixture using avian myeloblastosis virus reverse transcriptase (Promega, Madison, WI) and SEQ ID NO:104 as a primer. The resulting cDNA was amplified in a "nested" PCR assay by *Taq* DNA polymerase (Amplitaq, Perkin-Elmer/Cetus) as described previously (Bukh et al. (1992a)) with primer set *e* (SEQ ID NOs:103-106). Precautions were taken to avoid contamination with exogenous HCV nucleic acid (Bukh et al. 1992a)), and negative controls (normal, uninfected serum) were interspersed between every test sample in both the RNA extraction and cDNA PCR procedures. No false positive results were observed in the analysis. In most instances,

amplified DNA (first or second PCR products) was reamplified with primers SEQ ID NO:107 and SEQ ID NO:108 prior to sequencing since these two primers contained EcoR1 sites which would facilitate future cloning of the E1 gene. Amplified DNA was purified by gel electrophoresis followed by glass-milk extraction (Geneclean, BIO 101, LaJolla, CA) and both strands were sequenced directly by the dideoxy-nucleotide chain termination method (Bachman, B. et al. (1990) Nucl. Acids Res. 18:1309)) with phage T7 DNA polymerase (Sequenase, United States Biochemicals, Cleveland, OH), [alpha ^{35}S]dATP (Amersham, Arlington Heights, IL) or [alpha ^{33}P] dATP (Amersham or DuPont, Wilmington, DE) and sequencing primers. RNA extracted from serum containing HCV strain H-77, previously sequenced by Ogata, N. et al. (1991), was amplified with primer set e (SEQ ID NOs:103-106) and sequenced in parallel as a control. The nucleotide sequences of the envelope 1 (E1) gene of all 51 HCV isolates are shown as SEQ ID NOs:1 - 51. In all 51 HCV isolates, the E1 gene was exactly 576 nucleotides in length and did not have any in-frame stop codons.

Example 2

Computer Analysis of the Nucleotide and Deduced Amino Acid Sequences of the E1 Gene of the 51 HCV Isolates

Multiple computer-generated alignments of the nucleotide (SEQ ID NOs:1-51, Figures 1A-H) and deduced amino acid sequences (SEQ ID NOs:52-102, Figures 2A-H) of the cDNAs of the 51 HCV isolates constructed using the computer program GENALIGN (Miller, R.H. et al. (1990) Proc. Natl. Acad. Sci. USA 87:2057-2061) resulted in the 51 HCV isolates being divided into twelve genotypes based upon the degree of variation of the E1 gene sequence as shown in table 1.

Biochemistry: Bukh *et al.*

Table 1. Percent nucleotide (nt) and amino acid (aa) sequence identify of the E1 gene among the 12 HCV genotypes.

	I/1a	II/1b	III/2a	IV/2b	2c	(V)/3a	4a	4b	4c	4d	5a	6a	nt:
	89.9-97.6	72.0-76.2	59.2-63.7	56.1-58.3	60.8-62.8	63.0-66.3	63.9-67.2	64.9-66.8	62.7-64.4	67.7-69.4	62.3-67.2	62.2-63.9	I/1a
aa:		88.9-97.9	58.3-62.2	53.8-57.5	60.1-61.5	63.9-67.2	60.9-63.7	63.4-65.8	61.6-65.1	63.0-65.5	62.2-66.5	61.6-63.0	II/1b
I/1a	91.1-98.4		88.0-91.3	69.1-71.0	72.7-73.6	58.0-60.8	61.5-62.7	58.9-60.4	59.7-63.4	58.7-61.3	56.6-60.8	55.0-56.8	III/2a
II/1b	75.5-80.7	90.1-97.9		92.7-95.0	67.5-68.9	56.3-58.3	58.9-60.8	56.4-57.6	57.1-59.9	57.5-59.0	53.5-56.6	53.6-55.2	IV/2b
III/2a	58.3-64.6	52.6-56.8	89.1-92.7		---	57.5-58.2	59.2	58.5	58.0-58.3	58.9	56.9-57.1	57.6	2c
IV/2b	54.2-56.8	51.0-54.2	69.3-72.9	93.8-96.4		93.8-99.1	64.4-65.3	62.7-64.1	60.9-62.5	62.3-63.9	61.8-64.4	58.0-58.9	(V)/3a
2c	56.3-60.4	52.6-55.7	74.5-77.1	67.7-69.8	---		---	74.8	75.5-78.0	74.8	62.8-64.6	62.0	4a
(V)/3a	64.1-68.8	66.7-70.8	54.7-58.9	54.2-56.8	52.1-53.6	94.3-98.4		---	74.0-74.8	72.0	63.9-64.6	62.7	4b
4a	69.3-73.4	64.6-67.2	62.0-63.0	58.9-60.4	58.3	66.1-68.8	---		90.1	77.6-78.6	62.7-64.8	63.0-64.4	4c
4b	66.7-69.3	66.1-70.3	53.6-56.3	52.1-53.1	53.6	62.0-64.6	76.0	---		---	64.4-66.1	64.1	4d
4c	66.1-72.9	64.6-69.3	55.2-61.5	54.2-58.3	54.7-58.3	63.0-65.6	77.1-81.3	79.2-80.2	89.6		90.1-95.7	60.6-63.2	5a
4d	73.4-75.5	66.7-70.3	56.3-58.9	55.2-55.7	54.2	63.5-64.6	78.1	77.6	82.8	---		---	6a
5a	66.1-73.4	64.1-70.3	52.6-57.3	50.5-53.1	54.2-56.3	60.4-64.1	67.2-68.2	65.1-67.2	67.7-71.4	69.3-71.4	92.7-97.4		
6a	64.6-65.6	62.5-65.6	49.0-51.0	49.0-50.5	50.5	57.8-58.9	66.1	62.5	66.1-67.2	66.7	62.0-63.5	---	

Nucleotide sequences analyzed in compiling the above table are shown in SEQ ID NOs:1-51 while the amino acid sequences analyzed are shown in SEQ ID NOs:52-102. The grouping of SEQ ID NOs: into genotypes is previously described in the specification.

The nucleotide and amino acid sequence identity of HCV isolates of the same genotype was in the range of 88.0-99.1% and 89.1-98.4%, respectively, whereas that of HCV isolates of different genotypes was in the range of 53.5-78.6% and 49.0-82.8%, respectively. The latter differences are similar to those found when comparing the envelope gene sequences of the various serotypes of the related flaviviruses, as well as other RNA viruses. When microheterogenicity in a sequence was observed, defined as more than one prominent nucleotide at a specific position, the nucleotide that was identical to that of the HCV prototype (HCV1, Choo et al. (1989)) was reported if possible. Alternatively, the nucleotide that was identical to the most closely related isolate is shown.

Analysis of the consensus sequence of the E1 protein of the 51 HCV isolates from this study demonstrated that a total of 60 (30.3%) of the 192 amino acids of the E1 protein were invariant among these isolates (Fig. 3). Most impressive, all 8 cysteine residues as well as 6 of 8 proline residues were invariant. The most abundant amino acids (e.g. alanine, valine and leucine) showed a very low degree of conservation. The consensus sequence of the E1 protein contained 5 potential N-linked glycosylation sites. Three sites at positions 209, 305 and 325 were maintained in all 51 HCV isolates. A site at position 196 was maintained in all isolates except the sole isolate of genotype 2c. Also, a site at position 234 was maintained in all isolates except one isolate of genotype I/1a, all four isolates of genotype IV/2b and the sole isolate of genotype 6a. Conversely, only genotype IV/2b isolates had a potential glycosylation site at position 233. Further analysis revealed a highly conserved amino acid domain (aa 302-328) in the E1 protein with 20 (74.1%) of 27 amino acids invariant among all 51 HCV isolates. It is possible that the 5' and 3' ends of this domain are conserved due to important cysteine residues and N-linked glycosylation

sites. The central sequence, 5'-GHRMAWDMM-3' (aa 315-323), may be conserved due to additional functional constraints on the protein structure. Finally, although the amino acid sequence surrounding the putative E1 protein cleavage site was variable, an amino acid doublet (GV) at position 380 was invariant among all HCV isolates.

A dendrogram of the genetic relatedness of the E1 protein of selected HCV isolates representing the 12 genotypes is shown in Fig. 4. This dendrogram was constructed using the program CLUSTAL (Weiner, A.J. et al. (1991) Virology 180:842-848) and had a limit of 25 sequences. The scale showing percent identity was added based upon manual calculation. From the 51 HCV isolates for which the complete sequence of the E1 gene region was obtained, 25 isolates representing the twelve genotypes were selected for analysis as follows. Among isolates with genotype I/1a (SEQ ID NOs:52-59), as well as among isolates with genotype II/1b (SEQ ID NOs:60-76) the two isolates with the lowest amino acid identity within each genotype were included. Among isolates of genotype IV/2b, isolate DK8 (SEQ ID NO:81) that has an amino acid identity of 96.4% to isolate T8 (SEQ ID NO:84) was excluded. Among isolates of genotype V/3a, isolates S2 (SEQ ID NO:88) and S54 (SEQ ID NO:90) that both shared 97.9 % of the amino acids of isolates HK10 (SEQ ID NO:87) and S52 (SEQ ID NO:89) were excluded. Finally, among isolates of genotype VI, isolates SA4 (SEQ ID NO:97) and SA5 (SEQ ID NO:98) with an amino acid identity to isolate SA7 (SEQ ID NO:100) of 96.4% and 95.8%, respectively were excluded. This dendrogram in combination with the analysis of the E1 gene sequence of 51 HCV isolates in Table 1 demonstrates extensive heterogeneity of this important gene.

The worldwide distribution of the 12 genotypes among 74 HCV isolates is depicted in Fig. 5. The complete E1 gene sequence was determined in 51 of these HCV isolates (SEQ ID NOs:1-51), including 8 isolates of genotype I/1a,

17 isolates of genotype II/1b and 26 isolates comprising genotypes III/2a, IV/2b, 2c, 3a, 4a-4d, 5a and 6a. In the remaining 23 isolates, all of genotypes I/1a and II/1b, the genotype assignment was based on a partial E1 gene sequence since they did not represent additional genotypes in any of the 12 countries. The number of isolates of a particular genotype is given in each of the 12 countries studied. Of the twelve genotypes, genotypes I/1a and II/1b were the most common accounting for 48 (65%) of the 74 isolates. Analysis of the E1 gene sequences available in the GenBank data base at the time of this study revealed that all 44 such sequences were of genotypes I/1a, II/1b, III/2a and IV/2b. Thus, based upon E1 gene analysis, 8 new genotypes of HCV have been identified.

Also of interest, different HCV genotypes were frequently found in the same country, with the highest number of genotypes (five) being detected in Denmark. Of the twelve genotypes, genotypes I/1a, II/1b, III/2a, IV/2b and V/3a were widely distributed with genotype II/1b being identified in 11 of 12 countries studied (Zaire was the only exception). In addition, while genotypes I/1a and II/1b were predominant in the Americas, Europe and Asia, several new genotypes were predominant in Africa.

It was also found that genotypes I/1a, II/1b, III/2a, IV/2b and V/3a of HCV were widely distributed around the world, whereas genotypes 2c, 4a, 4b, 4d, 5a and 6a were identified only in discreet geographical regions. For example, the majority of isolates in South Africa comprised a new genotype (5a) and all isolates in Zaire comprised 3 new closely related genotypes (4a, 4b, 4c). These genotypes were not identified outside Africa.

Example 3

Detection by ELISA Based on Antigen from Insect Cells Expressing Complete E1 Protein

Expression of E1 protein in SF9 cells. A cDNA

(SEQ ID NO:1) encoding the complete E1 protein of SEQ ID NO:52 is subcloned into pBlueBac - Transfer vector (Invitrogen) using standard subcloning procedures. The resultant recombinant expression vector is cotransfected into SF9 insect cells (Invitrogen) by the Ca precipitation method according to the Invitrogen protocol.

ELISA Based on Infected SF9 cells. 5×10^6 SF9 cells infected with the above-described recombinant expression vector are resuspended in 1 ml of 10 mM Tris-HCl, pH 7.5, 0.15M NaCl and are then frozen and thawed 3 times. 10 ul of this suspension is dissolved in 10 ml of carbonate buffer (pH 9.6) and used to cover one flexible microtiter assay plate (Falcon). Serum samples are diluted 1:20, 1:400 and 1:8000, or 1:100, 1:1000 and 1:10000. Blocking and washing solutions for use in the ELISA assay are PBS containing 10% fetal calf serum and 0.5% gelatin (blocking solution) and PBS with 0.05% Tween -20 (Sigma, St.Louis, MO) (washing solution). As a secondary antibody, peroxidase-conjugated goat IgG fraction to human IgG or horse radish peroxidase-labelled goat anti-Old or anti-New World monkey immunoglobulin is used. The results are determined by measuring the optical density (O.D.) at 405 nm.

To determine if insect cells-derived E1 protein representing genotype I/a of HCV could detect anti-HCV antibody in chimpanzees infected with genotype I/1a of HCV, three infected chimpanzees are examined. The serum of all 3 chimpanzees are found to seroconvert to anti-HCV.

Example 4

Use of the Complete E1 Protein as a Vaccine

Mammals are immunized with purified or partially purified E1 protein in an amount sufficient to stimulate the production of protective antibodies. The immunized mammals challenged with various genotypes of HCV are

protected.

It is understood by one skilled in the art that the recombinant E1 protein used in the above vaccine can also be used in combination with other recombinant E1 proteins having an amino acid sequence shown in SEQ ID NOs:52-102.

Example 5

Determination of the Genotype of an HCV Isolate Via Hybridization of Genotype-Specific Oligonucleotides to RT-PCR Amplification Products.

Viral RNA is isolated from serum obtained from a mammal and is subjected to RT-PCR as in Example 1. Following amplification, the amplified DNA is purified as described in Example 1 and aliquots of 100 mg of amplification product are applied to twelve dots on a nitrocellulose filter set in a dot blot apparatus. The twelve dots are then cut into separate dots and each dot is hybridized to a ^{32}p-labelled oligonucleotide specific for a single genotype of HCV. The oligonucleotides to be used as hybridization probes are selected from SEQ ID NOs:109-135.

Example 6

ELISA Based on Synthetic Peptides Derived From E1 cDNA Sequences

Synthetic peptides specific for genotype I/1a and having amino acid sequences according to SEQ ID NOs:136-148 are placed in 0.1% PBS buffer and 50ul of 1mg/ml of peptide is used to cover each well of the microtiter assay plate. Serum samples from two mammals infected with genotype I/1a HCV and from one mammal infected with genotype 5a HCV are diluted as in Example 3 and the ELISA is carried out as in Example 3. Both mammals infected with genotype I HCV react positively with peptides while the mammal infected with genotype 5a HCV exhibit no reactivity.

Example 7

Use of the E1 Peptides as a Vaccine

Since the E1 genotype-specific peptides of the present invention are derived from two variable regions in the complete E1 protein, there exists support for the use of these peptides as a vaccine to protect against a variety of HCV genotypes. Mammals are immunized with peptide(s) selected from SEQ ID NOs: 136-159 in an amount sufficient to stimulate production of protective antibodies. The immunized mammals challenged with various genotypes of HCV are protected.

(1) GENERAL INFORMATION:

(i) APPLICANTS: BUKH, J., MILLER, R.H. AND PURCELL, R.H.

(ii) TITLE OF INVENTION: NUCLEOTIDE AND DEDUCED AMINO ACID SEQUENCES OF THE ENVELOPE 1 GENE OF 51 ISOLATES OF HEPATITIS C AND THE USE OF REAGENTS DERIVED FROM THESE SEQUENCES IN DIAGNOSTIC METHODS AND VACCINES

(iii) NUMBER OF SEQUENCES: 159

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(v) COMPUTER READABLE FORM:
(A) MEDIUM TYPE: FLOPPY DISK
(B) COMPUTER: IBM PC COMPATIBLE
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: WORDPERFECT 5.1

(vi) CURRENT APPLICATION DATA:
(A) APPLICATION NUMBER: PCT/US94/_____
(B) FILING DATE: 28-JUN-1994
(C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: 08/086,428
(B) FILING DATE: 29-JUN-1993

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(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 576 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(vi) ORIGINAL SOURCE:
(A) ORGANISM: homosapiens
(C) INDIVIDUAL ISOLATE: DK7

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

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TAC CAA GTG CGC AAC TCC ACG GGG CTT TAC CAT GTC ACC      39
AAT GAT TGC CCT AAC TCG AGT ATC GTG TAC GAG GCG GCC      78
GAT GCC ATC CTG CAC ACT CCG GGG TGT GTC CCT TGC GTT     117
CGC GAG GGT AAC GTC TCG AGG TGT TGG GTG GCG ATG ACC     156
CCC ACG GTG GCC ACC AGG GAT GGC AAA CTC CCC ACA GCG     195
CAG CTT CGA CGT CAC ATC GAT CTG CTC GTC GGG AGT GCC     234
ACC CTC TGT TCG GCC CTC TAC GTG GGG GAC CTG TGC GGG     273
TCT GTC TTT CTT GTC GGT CAA CTG TTT ACC TTC TCT CCC     312
AGG CGC CAC TGG ACG ACG CAA GGC TGC AAT TGT TCT ATC     351
TAT CCT GGC CAT ATA ACG GGT CAC CGC ATG GCG TGG GAT     390
ATG ATG ATG AAC TGG TCC CCT ACC ACG GCG TTG GTA GTA     429
GCT CAG CTG CTC CGG ATC CCG CAA GCC ATC TTG GAC ATG     468
ATC GCT GGT GCT CAC TGG GGA GTC CTG GCG GGC ATA GCG     507
TAT TTT TCC ATG GTG GGG AAC TGG GCG AAG GTC CTG GTA     546
GTG CTG CTG CTA TTT GCC GGC GTC GAC GCG                 576
```

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 576 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(vi) ORIGINAL SOURCE:
(A) ORGANISM: homosapiens
(C) INDIVIDUAL ISOLATE: DK9

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

```
TAC CAA GTA CGC AAC TCC TCG GGC CTC TAC CAT GTC ACC      39
AAT GAT TGC CCT AAC TCG AGT ATT GTG TAC GAG GCG GCC      78
GAT GCC ATC CTG CAT TCT CCA GGG TGT GTC CCT TGC GTT     117
CGC GAG GGT AAC GCC TCG AAA TGT TGG GTG GCG GTG GCC     156
CCC ACG GTG GCC ACC AGG GAC GGC AAG CTC CCC GCA ACG     195
CAG CTT CGA CGT CAC ATC GAT CTG CTT GTC GGG AGC GCC     234
ACC CTC TGC TCG GCC CTC TAT GTG GGG GAC TTG TGC GGG     273
TCT GTC TTC CTT GTC GGC CAA CTG TTC ACC TTC TCC CCC     312
AGA CGC CAC TGG ACA ACG CAA GAC TGC AAC TGT TCT ATC     351
TAC CCC GGC CAT ATT ACG GGT CAT CGC ATG GCG TGG GAT     390
ATG ATG ATG AAC TGG TCC CCT ACA GCA GCG CTG GTA ATG     429
GCG CAG CTG CTC AGG ATC CCG CAG GCC ATC TTG GAC ATG     468
ATC GCT GGT GCC CAC TGG GGA GTC CTA GCG GGC ATA GCG     507
TAT TTC TCC ATG GTG GGG AAC TGG GCG AAG GTC GTG GTG     546
GTA CTG TTG CTG TTT ACC GGC GTC GAT GCG                 576
```

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 576 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(vi) ORIGINAL SOURCE:
(A) ORGANISM: homosapiens
(C) INDIVIDUAL ISOLATE: DR1

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

```
CAC CAA GTG CGC AAC TCT ACA GGG CTT TAC CAT GTC ACC      39
AAT GAT TGC CCT AAT TCG AGT ATT GTG TAC GAG GCG GCC      78
GAT GCC ATC CTG CAC GCG CCG GGG TGT GTC CCT TGC GTT     117
CGC GAG GGT AAC GCC TCG AGG TGT TGG GTG GCG GTG ACC     156
CCC ACG GTG GCC ACC AGG GAC GGC AAA CTC CCC ACA ACG     195
CAG CTT CGA CGT CAC ATC GAC CTG CTT GTC GGG AGC GCC     234
ACC CTC TGC TCG GCC CTC TAC GTG GGG GAC CTG TGC GGG     273
TCT GTC TTC CTT GTC GGT CAA CTG TTC ACC TTT TCT CCC     312
AGG CGC CAC TGG ACA ACG CAA GAC TGC AAT TGT TCT ATC     351
TAT CCC GGC CAT ATA ACG GGA CAC CGT ATG GCA TGG GAT     390
ATG ATG ATG AAC TGG TCC CCT ACG ACA GCG CTG GTA ATG     429
GCT CAG CTG CTC CGG ATC CCA CAA GCC ATC TTG GAC ATG     468
ATC GCT GGA GCC CAC TGG GGA GTC CTA GCG GGC ATA GCG     507
TAT TTC TCC ATG GTG GGG AAC TGG GCG AAG GTC GTG GTA     546
GTG CTG TTG CTG TTT GCC GGC GTT GAT GCG                 576
```

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 576 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(vi) ORIGINAL SOURCE:
(A) ORGANISM: homosapiens
(C) INDIVIDUAL ISOLATE: DR4

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

```
CAC CAA GTG CGC AAC TCT ACA GGG CTT TAC CAT GTC ACC      39
AAT GAT TGC CCT AAT TCG AGT ATT GTG TAC GAG GCG GCC      78
GAT GCC ATC CTG CAC ACG CCG GGG TGT GTC CCT TGC GTT     117
CGC GAG GGT AAC ACC TCG AGG TGT TGG GTG GCG GTG ACC     156
CCC ACG GTG GCC ACC AGG GAC GGC AAA CTC CCC ACA ACG     195
CAG CTC CGA CGT CAC ATC GAC CTG CTT GTC GGG AGC GCC     234
ACC CTC TGC TCG GCC CTC TAC GTG GGG GAC TTG TGC GGG     273
TCT GTC TTC CTT GTC GGT CAA CTG TTC ACC TTC TCT CCC     312
AGG CAC CAC TGG ACA ACG CAA GAC TGC AAT TGT TCC ATC     351
```

TAT CCC GGC CAT ATA ACG GGC CAC CGC ATG GCG TGG GAT 390
ATG ATG ATG AAC TGG TCC CCT ACG ACA GCG CTG GTA GTA 429
GCT CAG CTG CTC CGG ATC CCA CAA GCC ATC TTG GAC ATG 468
ATC GCT GGT GCC CAC TGG GGA GTC CTA GCG GGC ATA GCG 507
TAT TTC TCC ATG GTG GGG AAC TGG GCG AAG GTC CTG GTA 546
GTG CTG TTG CTG TTT GCC GGC GTT GAT GCG 576

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 576 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(vi) ORIGINAL SOURCE:
(A) ORGANISM: homosapiens
(C) INDIVIDUAL ISOLATE: S14

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

TAC CAA GTG CGC AAC TCC ACG GGG CTT TAC CAT GTT ACC 39
AAT GAT TGC CCT AAC TCG AGT ATT GTG TAC GAG ACA GCT 78
GAT GCT ATC CTA CAC GCT CCG GGA TGT GTC CCT TGC GTT 117
CGT GAG GGT AAC ACC TCG AGG TGT TGG GTG GCG ATG ACC 156
CCC ACG GTG GCC ACC AGG GAC GGC AAA CTC CCC GCA ACG 195
CAG CTT CGA CGT TAC ATC GAT CTG CTT GTC GGG AGC GCC 234
ACC CTC TGT TCG GCC CTC TAC GTG GGG GAC TTG TGC GGG 273
TCT GTC TTT CTT GTC GGT CAG CTG TTT ACC TTC TCT CCC 312
AGG CGC CTC TGG ACG ACG CAA GAC TGC AAT TGT TCT ATC 351
TAT CCC GGC CAT ATA ACG GGT CAT CGC ATG GCA TGG GAT 390
ATG ATG ATG AAC TGG TCC CCT ACG ACG GCA CTG GTA GTA 429
GCT CAG CTG CTC CGG ATC CCA CAA GCC ATC TTG GAT ATG 468
ATC GCT GGT GCT CAC TGG GGA GTC CTA GCG GGC ATA GCG 507
TAT TTC TCC ATG GTG GGA AAC TGG GCG AAG GTC CTA GTG 546
GTG CTG CTG CTA TTC GCC GGC GTT GAC GCG 576

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 576 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(vi) ORIGINAL SOURCE:
(A) ORGANISM: homosapiens
(C) INDIVIDUAL ISOLATE: S18

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

TAC CAA GTA CGC AAC TCC ACG GGC CTT TAC CAT GTC ACC 39

```
AAT GAC TGC CCT AAC TCG AGC ATT GTG TAC GAG ACG GCC        78
GAT ACC ATC CTA CAC TCT CCG GGG TGT GTC CCT TGC GTT       117
CGC GAG GGT AAC GCC TCG AGA TGT TGG GTG CCG GTG GCC       156
CCC ACA GTT GCC ACC AGG GAC GGC AAA CTC CCC GCA ACG       195
CAG CTT CGA CGT CAC ATC GAT CTG CTT GTT GGG AGC GCC       234
ACC CTC TGC TCG GCC CTC TAT GTG GGG GAC CTG TGC GGG       273
TCT GTC TTT CTT GTC AGC CAG CTG TTC ACT ATC TCC CCC       312
AGG CGC CAC TGG ACA ACG CAA GAC TGC AAC TGT TCT ATC       351
TAC CCC GGC CAT ATA ACG GGT CAC CGT ATG GCA TGG GAT       390
ATG ATG ATG AAC TGG TCC CCT ACA ACG GCG TTG GTA ATA       429
GCT CAG CTG CTC AGG GTC CCG CAA GCC GTC TTG GAC ATG       468
ATC GCT GGT GCC CAC TGG GGA GTC CTA GCG GGC ATA GCG       507
TAT TTC TCC ATG GCG GGG AAC TGG GCG AAG GTC CTG CTA       546
GTG CTG TTG CTG TTT GCC GGC GTC GAT GCG                  576
```

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 576 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(vi) ORIGINAL SOURCE:
(A) ORGANISM: homosapiens
(C) INDIVIDUAL ISOLATE: SW1

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

```
TAC CAA GTA CGC AAC TCC TCG GGC CTT TAC CAT GTC ACC        39
AAT GAT TGC CCT AAC TCG AGT ATT GTG TAC GAG ACG GCC        78
GAT GCC ATT CTA CAC TCT CCA GGG TGT GTC CCT TGC GTT       117
CGC GAG GAT GGC GCC CCG AAG TGT TGG GTG GCG GTG GCC       156
CCC ACA GTC GCC ACT AGG GAC GGC AAA CTC CCT GCA ACG       195
CAG CTT CGA CGT CAC ATC GAT CTG CTT GTC GGA AGC GCC       234
ACC CTC TGC TCG GCC CTC TAC GTG GGG GAC TTG TGC GGG       273
TCT GTC TTT CTC GTC AGT CAA CTG TTC ACG TTC TCC CCC       312
AGG CGC CAC TGG ACA ACG CAA GAC TGT AAC TGT TCT ATC       351
TAT CCC GGC CAC ATA ACG GGT CAC CGC ATG GCA TGG GAT       390
ATG ATG ATG AAC TGG TCC CCC ACA ACA GCG CTG GTA GTA       429
GCT CAG CTG CTC AGG ATC CCG CAA GCC GTC TTG GAC ATG       468
ATC GCT GGT GCC CAC TGG GGA GTC CTA GCG GGC ATA GCG       507
TAT TTC TCC ATG GTG GGG AAC TGG GCG AAG GTC CTG ATA       546
GTG CTG TTG CTG TTT TCC GGC GTC GAT GCG                  576
```

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 576 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(vi) ORIGINAL SOURCE:
(A) ORGANISM: homosapiens
(C) INDIVIDUAL ISOLATE: US11

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

```
TAC CAA GTA CGC AAC TCC ACG GGG CTT TAC CAT GTC ACC      39
AAT GAT TGC CCT AAC TCG AGT ATT GTG TAC GAG GCG GCC      78
GAT GCC ATC CTG CAC ACT CCG GGG TGT GTT CCT TGC GTT     117
CGC GAG GGT AAC GCT TCG AGG TGT TGG GTG GCG ATG ACC     156
CCC ACG GTG GCC ACC AGG GAC GGC AAA CTC CCC ACA ACG     195
CAA CTT CGA CGT CAC ATC GAT CTG CTT GTC GGG AGC GCC     234
ACC CTC TGT TCG GCC CTC TAC GTG GGG GAC CTG TGC GGG     273
TCT GTC TTT CTT GTC GGT CAA CTG TTT ACC TTC TCT CCC     312
AGA CGC CAC TGG ACG ACG CAG GGC TGC AAT TGT TCT ATC     351
TAT CCC GGC CAT ATA ACG GGT CAC CGC ATG GCA TGG GAT     390
ATG ATG ATG AAC TGG TCC CCT ACG GCG GCG TTG GTG GTA     429
GCT CAG CTG CTC CGG ATC CCA CAA GCC ATC TTG GAC ATG     468
ATC GCT GGT GCT CAC TGG GGA GTC CTA GCG GGC ATA GCG     507
TAT TTC TCC ATG GTG GGG AAC TGG GCG AAG GTC CTG GTA     546
GTG CTG CTG CTA TTT GCC GGC GTC GAC GCG                 576
```

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 576 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(vi) ORIGINAL SOURCE:
(A) ORGANISM: homosapiens
(C) INDIVIDUAL ISOLATE: D1

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

```
TAT GAA GTG CGC AAC GTG TCC GGG GTG TAC CAT GTC ACG      39
AAC GAC TGT TCC AAC TCG AGC ATT GTG TAT GAG ACA GCG      78
GAC ATG ATC ATG CAC ACC CCC GGG TGC GTG CCC TGC GTT     117
CGG GAG GAC AAC TCC TCT CGC TGC TGG GTA GCG CTC ACC     156
CCC ACG CTC GCG GCT AGG AAT GGC AAC GTC CCC ACT ACG     195
GCG ATA CGA CGC CAC GTC GAT TTG CTC GTT GGG GCG GCT     234
GCT TTC TGC TCC GCC ATG TAC GTG GGG GAT CTC TGC GGA     273
TCT GTT TTC CTC ATC TCC CAG CTG TTC ACC CTC TCG CCT     312
CGC CGG CAT GAG ACG GTA CAG GAG TGT AAT TGC TCA ATC     351
TAT CCC GGC CAC GTG ACA GGT CAC CGT ATG GCT TGG GAT     390
ATG ATG ATG AAC TGG TCA CCT ACA ACA GCC TTA GTG GTA     429
TCG CAG TTA CTC CGG ATC CCA CAA GCT GTC ATG GAC ATG     468
GTG GCG GGG GCC CAC TGG GGG GTC CTG GCG GGC CTC GCC     507
TAC TAT TCC ATG GTG GGG AAC TGG GCT AAG GTT TTG ATT     546
GTG ATG CTA CTC TTT GCT GGC GTT GAC GGC                 576
```

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 576 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(vi) ORIGINAL SOURCE:
(A) ORGANISM: homosapiens
(C) INDIVIDUAL ISOLATE: D3

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

```
TAT GAA GTG CGC AAC GTG TCC GGG GTG TAC CAA GTC ACC      39
AAT GAC TGT TCC AAC TCG AGC ATC GTG TAT GAG ACA GCG      78
GAC ATG ATC ATG CAC ACC CCC GGG TGC GTG CCC TGC GTT     117
CGG GAG GAC AAC TCC TCT CGC TGC TGG GTA GCG CTC ACC     156
CCC ACG CTC GCG GCT AGG AAT AGC AGC GTC CCC ACT ACG     195
ACA ATA CGA CGC CAC GTC GAT TTG CTC GTT GGG GCG GCT     234
GCT TTC TGC TCC GCC ATG TAC GTG GGG GAT CTT TGC GGA     273
TCT GTT TTC CTC GTC TCC CAG CTG TTC ACC TTC TCG CCT     312
CGC CGG CAT GAG ACA GTA CAG GAA TGT AAC TGC TCA ATC     351
TAT CCC GGC CAC GTG ACA GGT CAC CGC ATG GCT TGG GAT     390
ATG ATG ATG AAC TGG TCG CCT ACA GCA GCC CTA GTG GTA     429
TCG CAG TTA CTC CGG ATC CCA CAA GCT GTC GTG GAC ATG     468
GTG GCG GGG GCC CAC TGG GGG GTC CTG GCG GGC CTC GCC     507
TAC TAT TCC ATG GTG GGG AAC TGG GCT AAG GTT TTG ATT     546
GTG ATG CTA CTC TTT GCT GGC GTC GAC GGC                 576
```

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 576 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(vi) ORIGINAL SOURCE:
(A) ORGANISM: homosapiens
(C) INDIVIDUAL ISOLATE: DK1

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

```
TAT GAA GTG CGC AAC GTG TCC GGG GTG TAC CAC GTC ACA      39
AAC GAC TGC TCC AAC TCA AGC ATC GTG TAT GAG GCA GTG      78
GAC GTG ATC ATG CAT ACC CCA GGG TGC GTG CCC TGC GTT     117
CGG GAG AAC AAC CAC TCC CGT TGC TGG GTA GCG CTC ACC     156
CCC ACG CTC GCG GCC AGG AAC GCC AGC ATC CCC ACT ACG     195
ACA ATA CGA CGC CAT GTC GAT TTG CTC GTT GGG GCG GCT     234
GCT TTC TGC TCC GCT ATG TAC GTG GGG GAC CTC TGC GGA     273
TCC GTT TTC CTC GTC TCT CAG CTG TTC ACC TTT TCA CCT     312
CGC CGG CAT GAG ACA GCA CAG GAC TGC AAC TGC TCA ATC     351
TAT CCC GGC CAC GTT TCA GGT CAC CGC ATG GCT TGG GAT     390
ATG ATG ATG AAC TGG TCA CCT ACA ACA GCC CTA GTG CTA     429
```

TCG CAG TTA CTC CGA ATC CCA CAA GCT GTC GTG GAC ATG 468
GTG GCG GGG GCC CAC TGG GGA GTC CTG GCG GGC CTC GCC 507
TAC TAC TCC ATG GCG GGG AAC TGG GCC AAG GTT TTA ATT 546
GTG TTG CTA CTC TTT GCC GGC GTT GAT GGG 576

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 576 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(vi) ORIGINAL SOURCE:
(A) ORGANISM: homosapiens
(C) INDIVIDUAL ISOLATE: HK3

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

TAT GAA GTG CGC AAC GTG TCC GGG ATA TAC CAT GTC ACG 39
AAC GAC TGC TCC AAC TCA AGC GTC GTG TAT GAG ACA GCA 78
GAC ATG ATC ATG CAT ACC CCT GGA TGC GTG CCC TGC GTA 117
CGG GAG AAC AAC TCC TCC CGC TGT TGG GTA GCG CTC ACT 156
CCC ACG CTC GCG GCC AGG AAC GTC AGC GTC CCC ACC ACG 195
ACA ATA CGA CGT CAC GTC GAC TTG CTC GTT GGG GCG GCT 234
GCC TTC TGC TCC GCT ATG TAC GTG GGG GAT CTC TGC GGA 273
TCT GTT TTC CTT GTC TCC CAG CTG TTC ACC TTC TCG CCT 312
CGC CGA CAC GAG ACA GTA CAG GAC TGC AAC TGC TCA CTC 351
TAT CCC GGC CAC GTA TCA GGT CAC CGC ATG GCT TGG GAT 390
ATG ATG ATG AAC TGG TCC CCT ACA GCA GCC CTA GTG GTG 429
TCG CAA TTA CTC CGG ATC CCG CAA GCT GTC GTG GAC ATG 468
GTG GCG GGG GCC CAC TGG GGA GTC CTA GCG GGC CTT GCC 507
TAC TAT TCC ATG GTG GGA AAC TGG GCT AAG GTT TTG ATT 546
GTG ATG CTA CTT TTT GCC GGC GTT GAT GGG 576

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 576 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(vi) ORIGINAL SOURCE:
(A) ORGANISM: homosapiens
(C) INDIVIDUAL ISOLATE: HK4

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

CAT GAA GTG CAC AAC GTA TCC GGG ATC TAC CAT GTC ACG 39
AAC GAC TGC TCC AAC TCA AGT ATT GTG TAT GAG GCA GCG 78
GAC ATG ATC ATG CAT ACC CCC GGG TGC GTG CCC TGC GTC 117

```
CGG GAG AAC AAC TCC TCC CGT TGC TGG GTA GCG CTC ACT      156
CCC ACG CTC GCG GCC AGG AAC GCC AGC ATC CCC ACT ACG      195
ACA ATA CGA CGC CAT GTC GAC TTG CTC GTT GGG GCG GCT      234
GCT TTC TGC TCC GCC ATG TAC GTG GGA GAT CTC TGC GGA      273
TCT GTC TTC CTC GTC TCC CAG TTG TTC ACC TTC TCG CCT      312
CGC CGG CAT GAG ACG GTA CAG GAC TGC AAT TGC TCA ATC      351
TAT CCC GGC CAC GTA TCA GGT CAC CGC ATG GCT TGG GAT      390
ATG ATG ATG AAC TGG TCA CCT ACA GCA GCC CTA GTG GTA      429
TCG CAG TTA CTC CGA CTC CCA CAA GCT GTC ATG GAC ATG      468
GTG GCG GGA GCC CAC TGG GGA GTC CTA GCG GGC CTT GCT      507
TAC TAT TCC ATG GTG GGG AAC TGG GCC AAG GTT TTG ATT      546
GTG ATG CTA CTC TTT GCC GGC GTT GAC GGG                  576
```

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 576 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(vi) ORIGINAL SOURCE:
(A) ORGANISM: homosapiens
(C) INDIVIDUAL ISOLATE: HK5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

```
TAT GAA GTG CGC AAC GTG TCC GGG GTA TAC CAT GTC ACG       39
AAC GAC TGC TCC AAC TTA AGC ATC GTG TAC GAG ACA ACG       78
GAC ATG ATC ATG CAC ACC CCT GGG TGC GTG CCC TGC GTT      117
CGG GAA AAC AAC TCC TCC CGT TGT TGG GTA GCG CTC GCC      156
CCC ACG CTC GCG GCC AGG AAC GCC AGC GTC CCC ACC ACG      195
GCA ATA CGA CGC CAC GTC GAC TTG CTC GTT GGG GCG GCT      234
GCT TTC TGC TCC GCT ATG TAC GTG GGG GAT CTT TGC GGA      273
TCT GTT TTC CTC GTC TCC CAG CTG TTC ACC TTC TCG CCT      312
CGC CGA CAC GAG ACG GTA CAG GAC TGC AAC TGC TCA ATC      351
TAT CCC GGC CAC GTA ACA GGT CAC CGC ATG GCT TGG GAT      390
ATG ATG ATG AAC TGG TCA CCT ACA ACA GCC CTA GTG GTG      429
TCG CAG TTA CTC CGG ATC CCG CAA GCT GTC GTG GAC ATG      468
GTA GCG GGG GCC CAC TGG GGG GTC CTG GCG GGC CTT GCC      507
TAC TAT TCC ATG GTG GGA AAC TGG GCT AAG GTT TTG ATT      546
GTG ATG CTA CTT TTT GCC GGC GTT GAT GGG                  576
```

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 576 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(vi) ORIGINAL SOURCE:

(A) ORGANISM: homosapiens
(C) INDIVIDUAL ISOLATE: HK8

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

```
TAT GAA GTG CGC AAC GTG TCC GGG ATA TAC CAT GTC ACG      39
AAC GAC TGC TCC AAC TCA AGC ATC GTG TAT GAA ACA GCG      78
GAC ATG ATT ATG CAT ACC CCT GGA TGC ATG CCC TGC GTT     117
CGG GAG AAC AAC TCC TCC CGT TGC TGG GTG GCG CTC ACT     156
CCC ACG CTC GCG GCT AGG AAT GTC AGC GTC CCC ACT ACG     195
ACA ATA CGA CGC CAC GTC GAC TTG CTC GTT GGG GCG GCT     234
GCT TTC TGC TCC GCT ATG TAC GTG GGG GAT CTC TGC GGA     273
TCT GTT TTC CTC GTC TCC CAG CTG TTC ACC TTT TCG CCT     312
CGC CGA CAC GAG ACG GTA CAG GAC TGC AAC TGC TCA ATC     351
TAT CCC GGC CAC GTA TCA GGT CAC CGC ATG GCT TGG GAT     390
ATG ATG ATG AAC TGG TCG CCC ACA ACA GCC CTA GTG GTG     429
TCG CAG TTA CTC CGG ATC CCG CAA GCT ATC GTG GAC ATG     468
GTG GCG GGG GCC CAC TGG GGA GTC CTA GCG GGC CTT GCC     507
TAC TAT TCC ATG GTG GGC AAC TGG GCT AAG GTT TTG ATT     546
GTG ATG CTA CTG TTT GCC GGC GTT GAT GGG                 576
```

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 576 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(vi) ORIGINAL SOURCE:
(A) ORGANISM: homosapiens
(C) INDIVIDUAL ISOLATE: IND5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

```
TAT GAA GTG CGC AAC GTG TCC GGG GTG TAC CAT GTC ACG      39
AAC GAC TGC TCC AAC TCA AGT ATT GTG TAT GAG GCA GCG      78
GAC ATG ATC ATG CAC ACT CCC GGG TGC GTG CCC TGC GTT     117
CGG GAG GGC AAC TCC TCT CGC TGC TGG GTA GCG CTC ACT     156
CCC ACT CTC GCG GCC AGG AAC GCC AGC GTC TCC ACC ACG     195
ACA ATA CGA CAC CAC GTC GAT TTG CTC GTT GGG GCG GCT     234
GCT TTC TGT TCC GCT ATG TAC GTG GGG GAT CTA TGC GGA     273
TCT GTT TTC CTC GTC TCC CAG CTG TTC ACC TTC TCA CCG     312
CGC CGG CAT GAG ACA GTA CAG GAC TGC AAT TGC TCC ATC     351
TAT CCC GGC CAC GTA TCA GGT CAC CGC ATG GCC TGG GAT     390
ATG ATG ATG AAC TGG TCA CCT ACA GCA GCC CTA GTG GTA     429
TCG CAG TTG CTC CGG ATC CCA CAA GCT GTC GTG GAT ATG     468
GTG GCG GGG GCC CAC TGG GGA ATC CTG GCG GGC CTT GCC     507
TAC TAT TCC ATG GTA GGG AAC TGG GCT AAG GTT TTG ATT     546
GTG ATG CTA CTC TTT GCC GGC GTT GAC GGG                 576
```

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 576 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(vi) ORIGINAL SOURCE:
(A) ORGANISM: homosapiens
(C) INDIVIDUAL ISOLATE: IND8

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

```
TAT GAG GTG CGC AAC GTG TCC GGG GTG TAC CAT GTC ACG      39
AAC GAC TGC TCC AAC TCA AGT ATT GTG TAT GAG GCA GCG      78
GAC ATG ATC ATG CAC ACC CCC GGG TGC GTG CCC TGC GTT     117
CGG GAG GGC AAC TTC TCT AGT TGC TGG GTA GCG CTC ACT     156
CCC ACT CTC GCG GCT AGG AAC GCC AGC GTC CCC ACC ACG     195
ACA ATA CGA CGC CAC GTC GAT TTG CTC GTT GGG GCG GCT     234
GCT TTC TGT TCC GCT ATG TAC GTG GGG GAT CTC TGC GGA     273
TCT GTT TTC CTT GTC TCC CAG CTG TTC ACC TTC TCA CCG     312
CGC CGG CAT GAG ACA GTA CAG GAC TGC AAT TGC TCC ATC     351
TAT CCC GGC CAC GTA TCA GGT CAC CGC ATG GCT TGG GAT     390
ATG ATG ATG AAC TGG TCA CCT ACA GCG GCC CTA GTG GTA     429
TCG CAG TTG CTC CGG ATC CCA CAA GCT GTC GTG GAT ATG     468
GTG GCG GGG GCC CAC TGG GGA ATC CTG GCG GGC CTT GCC     507
TAC TAT TCC ATG GTA GGG AAC TGG GCT AAG GTT TTG ATT     546
GTG ATG CTA CTC TTT GCC GGC GTT GAC GGG                 576
```

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 576 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(vi) ORIGINAL SOURCE:
(A) ORGANISM: homosapiens
(C) INDIVIDUAL ISOLATE: P10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

```
TAT GAA GTG CGC AAC GTG TCC GGG GTG TAC CAT GTC ACG      39
AAC GAC TGC TCC AAC TCA AGT ATT GTG TAT GAG GCA GCG      78
GAC ATG ATA ATG CAC ACC CCC GGG TGC GTG CCC TGT GTT     117
CGG GAG AAC AAC TCC TCC CGC TGC TGG GTA GCG CTC ACT     156
CCC ACA CTC GCG GCT AGG AAT TCC AGC GTC CCA ACT ACG     195
GCA ATA CGA CGC CAT GTC GAT TTG CTC GTT GGG GCG GCT     234
GCT TTC TGC TCC GCT ATG TAC GTG GGG GAT CTC TGC GGA     273
TCT GTT CTC CTC GTC TCC CAG CTG TTC ACC TTC TCA CCT     312
CGC CGG CAT TGG ACA GTA CAG GAC TGC AAT TGT TCA ATC     351
TAT CCT GGC CAC GTA TCA GGT CAC CGC ATG GCT TGG GAT     390
ATG ATG ATG AAC TGG TCG CCC ACA GCA GCC CTA GTG GTG     429
```

TCG CAG CTA CTC CGG ATC CCA CAA GCT ATC TTG GAT GTG 468
GTG GCG GGG GCC CAC TGG GGA GTC CTG GCG GGC CTT GCC 507
TAC TAT TCC ATG GTG GGG AAC TGG GCT AAG GTC TTG ATT 546
GTG ATG CTA CTC TTT GCC GGC GTT GAC GGA 576

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 576 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(vi) ORIGINAL SOURCE:
(A) ORGANISM: homosapiens
(C) INDIVIDUAL ISOLATE: S9

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

TAT GAA GTG CGC AAC GTA TCC GGG GCG TAC CAT GTC ACG 39
AAC GAC TGC TCC AAC TCA AGT ATT GTG TAC GAG GCA GCG 78
GAC GTG ATC ATG CAT ACC CCC GGG TGT GTA CCC TGC GTT 117
CAG GAG GGT AAC TCC TCC CAA TGC TGG GTG GCG CTC ACC 156
CCC ACG CTC GCG GCC AGG AAC GCT ACC GTC CCC ACC ACG 195
ACA ATA CGA CGT CAT GTC GAT TTG CTC GTT GGG GCG GCT 234
GTT TTC TGC TCC GCT ATG TAC GTG GGG GAC CTG TGC GGA 273
TCT GTT TTC CTC ATC TCC CAG CTG TTC ACC ATC TCG CCC 312
CGT CGG CAT GAG ACA GTA CAG AAC TGC AAT TGC TCA ATC 351
TAT CCC GGA CAC GTG ACA GGT CAT CGC ATG GCC TGG GAT 390
ATG ATG ATG AAC TGG TCG CCT ACA ACA GCC CTA GTG GTA 429
TCG CAG CTA CTC CGG ATC CCA CAA GCT GTC ATG GAT ATG 468
GTG GCG GGG GCC CAC TGG GGA GTC CTG GCG GGC CTC GCC 507
TAC TAT TCC ATG GTG GGG AAC TGG GCT AAG GTT TTG ATT 546
GTG ATG CTA CTT TTT GCT GGT GTT GAC GGG 576

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 576 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(vi) ORIGINAL SOURCE:
(A) ORGANISM: homosapiens
(C) INDIVIDUAL ISOLATE: S45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

TAT GAA GTG CGC AAC GTG TCC GGG GCG TAC CAT GTC ACG 39
AAC GAC TGC TCC AAC TCA AGC ATT GTG TAT GAG GCA GTG 78
GAC GTG ATC CTG CAC ACC CCT GGG TGC GTG CCC TGC GTT 117

```
CGG GAG AAC AAC TCC TCC CGT TGC TGG GTG GCG CTC ACT      156
CCC ACG CTC GCG GCC AGG AAC TCC AGC GTC CCC ACT ACG      195
ACA ATA CGA CGT CAC GTC GAT TTG CTC GTT GGG GCG GCT      234
GCT TTC TGC TCC GCT ATG TAC GTG GGG GAT CTC TGC GGA      273
TCT GTT TTC CTT GTT TCC CAG CTG TTC ACC TTC TCG CCT      312
CGT CGG CAT GAG ACA GTA CAG GAC TGC AAC TGT TCA ATC      351
TAT CCC GGC CAC GTA ACA GGT CAC CGC ATG GCT TGG GAT      390
ATG ATG ATG AAC TGG TCG CCT ACA GCA GCC TTA GTG GTA      429
TCG CAG TTA CTC CGG ATC CCA CAA GCT GTC GTG GAC ATG      468
GTG GCG GGG GCC CAC TGG GGA GTC CTG GCG GGC CTT GCC      507
TAC TAT TCC ATG GTG GGG AAC TGG GCT AAG GTT CTG ATT      546
GTG ATG CTA CTC TTT GCC GGC GTT GAC GGG                 576
```

(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 576 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(vi) ORIGINAL SOURCE:
(A) ORGANISM: homosapiens
(C) INDIVIDUAL ISOLATE: SA10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

```
TAT GAA GTG CGC AAC GTG TCC GGG ATG TAC CAT GTC ACG       39
AAC GAC TGC TCC AAC TCA AGC ATT GTG TAT GAG GCA GCG       78
GAC ATG ATC ATG CAC ACC CCC GGG TGC GTG CCC TGC GTT      117
CGG GAG AAC AAC TCC TCC CGC TGC TGG GTA GCG CTC ACT      156
CCC ACG CTC GCG GCC AGG AAC TCC AGC GTC CCC ACT ACG      195
ACA ATA CGA CGC CAC GTC GAT TTG CTC GTT GGG GCG GCT      234
GCT TTC TGC TCC GCC ATG TAC GTG GGG GAC CTC TGC GGA      273
TCT GTT TTC CTT GTC TCC CAG CTG TTC ACC TTC TCG CCT      312
CGC CGG TAT GAG ACA GTA CAG GAC TGC AAT TGC TCA ATC      351
TAT CCC GGC CGC GTA ACA GGT CAC CGC ATG GCT TGG GAT      390
ATG ATG ATG AAC TGG TCA CCT ACA ACA GCT CTA GTA GTA      429
TCG CAG TTA CTC CGG ATC CCA CAA GCT ATC GTG GAC ATG      468
GTG GCG GGG GCC CAC TGG GGA GTC CTA GCG GGC CTT GCC      507
TAC TAT TCC ATG GTG GGG AAC TGG GCT AAG GTT TTG ATT      546
GTT ATG CTA CTC TTT GCC GGC GTT GAC GGG                 576
```

(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 576 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(vi) ORIGINAL SOURCE:

(A) ORGANISM: homosapiens
(C) INDIVIDUAL ISOLATE: SW2

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

```
TAT GAA GTG CGC AAC GTG TCC GGG GTG TAT CAT GTC ACG      39
AAC GAC TGT TCC AAC TCA AGC ATT GTG TAT GAG ACA GCG      78
GAC ATG ATC ATG CAT ACC CCC GGG TGC GTG CCC TGC GTT     117
CGG GAG GCC AAC TCC TCC CGC TGC TGG GTA GCG CTC ACT     156
CCC ACG CTA GCA GCC AGG AAC ACC AGC GTC CCC ACT ACG     195
ACA ATA CGA CGC CAC GTC GAT TTG CTC GTT GGG GCG GCT     234
GCT TTC TGC TCC GTT ATG TAC GTG GGG GAT CTC TGC GGA     273
TCT GTT TTC CTC GTC TCC CAG CTG TTC ACT TTT TCA CCT     312
CGC CGG CAC GAG ACA GTA CAG GAC TGC AAC TGT TCC ATC     351
TAT CCC GGC CAC GTA TCA GGT CAC CGC ATG GCT TGG GAC     390
ATG ATG ATG AAC TGG TCA CCT ACA GCA GCC CTG GTG GTA     429
TCG CAG TTA CTC CGG ATC CCA CAA GCT GTC GTG GAC ATG     468
GTA GCG GGG GCC CAC TGG GGA GTC CTG GCG GGC CTT GCA     507
TAC TAT TCC ATG GTG GGG AAC TGG GCT AAG GTT TTG ATT     546
GTG ATG CTA CTC TTT GCT GGC GTT GAC GGG                 576
```

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 576 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(vi) ORIGINAL SOURCE:
(A) ORGANISM: homosapiens
(C) INDIVIDUAL ISOLATE: T3

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

```
TAC GAA GTG CGC AAC GTG TCC GGG GTG TAC TAT GTC ACG      39
AAC GAC TGT TCC AAC TCA AGC ATT GTG TAT GAG ACA GCG      78
GAC ATG ATC ATG CAC ACC CCT GGG TGC GTG CCC TGC GTT     117
CGG GAG AGC AAT TCC TCC CGC TGC TGG GTA GCG CTT ACT     156
CCC ACG CTC GCG GCC AGG AAC GCC AGC GTC CCC ACT AAG     195
ACA ATA CGA CGT CAC GTC GAC TTG CTC GTT GGG GCG GCT     234
GCT TTC TGT TCC GCT ATG TAC GTG GGG GAT CTC TGC GGA     273
TCT GTT TTC CTC GTC TCC CAG CTG TTC ACT TTC TCG CCT     312
CGC CGG CAT GAG ACA GTA CAG GAC TGC AAC TGC TCA ATC     351
TAT CCC GGC CAC GTA ACA GGT CAC CGT ATG GCT TGG GAT     390
ATG ATG ATG AAC TGG TCG CCC ACA ACG GCA CTA GTG GTG     429
TCG CAG TTG CTC CGG ATC CCA CAA GCT GTC GTG GAC ATG     468
GTG GCG GGG GCC CAC TGG GGA GTC CTG GCG GGC CTT GCC     507
TAC TAT TCC ATG GTG GGG AAC TGG GCT AAG GTT TTG ATT     546
GTG CTG CTA CTC TTT GCC GGC GTT GAT GGG                 576
```

(2) INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 576 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(vi) ORIGINAL SOURCE:
(A) ORGANISM: homosapiens
(C) INDIVIDUAL ISOLATE: T10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

```
TAT GAA GTG CGC AAC GTG TCC GGG ATG TAC CAT GTC ACG      39
AAC GAC TGC TCC AAC TCA AGC ATT GTG TTT GAG GCA GCG      78
GAC TTG ATC ATG CAC ACC CCC GGG TGC GTG CCC TGC GTT     117
CGG GAG GGC AAC TCC TCC CGC TGC TGG GTA GCG CTC ACT     156
CCC ACG CTC GCG GCC AGG AAC ACC AGC GTC CCC ACT ACG     195
ACG ATA CGA CGC CAT GTC GAT TTG CTC GTT GGG GCG GCT     234
GCT TTC TGC TCC GCT ATG TAT GTG GGA GAC CTC TGC GGA     273
TCT GTT TTC CTC GTC TCT CAG CTG TTC ACC TTC TCG CCT     312
CGC CGG CAT GAG ACT TTG CAG GAC TGC AAC TGC TCA ATC     351
TAT CCC GGC CAT CTG TCA GGT CAC CGC ATG GCT TGG GAC     390
ATG ATG ATG AAC TGG TCG CCT ACA ACA GCT CTA GTG GTG     429
TCG CAG TTA CTC CGG ATC CCA CAA GCT GTC ATG GAC ATG     468
GTG ACA GGG GCC CAC TGG GGA GTC CTG GCG GGC CTT GCC     507
TAC TAT TCC ATG GCG GGG AAC TGG GCT AAG GTT TTA ATT     546
GTG ATG CTA CTC TTT GCC GGC GTT GAT GGG                 576
```

(2) INFORMATION FOR SEQ ID NO:25:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 576 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(vi) ORIGINAL SOURCE:
(A) ORGANISM: homosapiens
(C) INDIVIDUAL ISOLATE: US6

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

```
TAT GAA GTG CGC AAC GTG TCC GGG ATG TAC CAT GTC ACG      39
AAC GAC TGC TCC AAC TCA AGC ATT GTG TAT GAG GCA GCG      78
GAC ATG ATC ATG CAC ACT CCC GGG TGC GTG CCC TGT GTT     117
CGG GAG AAC AAT TCC TCC CGC TGC TGG GTA GCG CTC ACT     156
CCC ACG CTC GCG GCC AGG AAC GCT AGC GTC CCC ACT ACG     195
ACA ATA CGA CGC CAC GTC GAT TTG CTC GTT GGG GCG GCT     234
ACT TTC TGC TCC GCT ATG TAC GTG GGG GAC CTC TGC GGG     273
TCC GTT TTC CTC ATC TCC CAG CTG TTC ACC TTC TCG CCT     312
CGT CAG CAT GAG ACA GTA CAG GAC TGC AAT TGT TCA ATC     351
TAT CCC GGC CAC GTA TCA GGT CAC CGC ATG GCT TGG GAT     390
ATG ATG ATG AAT TGG TCA CCT ACA GCA GCC CTA GTG GTA     429
```

TCG CAG TTA CTC CGG ATC CCA CAA GCT GTC ATG GAC ATG 468
GTG GCG GGG GCC CAC TGG GGA GTC CTG GCG GGC CTT GCC 507
TAC TAT TCC ATG GTG GGG AAC TGG GCT AAG GTT CTG ATT 546
GTG TTG CTA CTC TTT GCC GGC GTT GAC GGG 576

(2) INFORMATION FOR SEQ ID NO:26:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 576 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(vi) ORIGINAL SOURCE:
(A) ORGANISM: homosapiens
(C) INDIVIDUAL ISOLATE: T2

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

GCC CAA GTG AGG AAC ACC AGC CGC GGT TAC ATG GTG ACT 39
AAC GAC TGT TCC AAT GAG AGC ATC ACC TGG CAG CTC CAA 78
GCC GCG GTT CTC CAC GTC CCC GGG TGT ATC CCG TGT GAG 117
AGG CTG GGA AAT ACA TCC CGA TGC TGG ATA CCG GTC ACA 156
CCA AAC GTG GCC GTG CGG CAG CCC GGC GCT CTT ACG CAG 195
GGC TTG CGG ACG CAC ATC GAC ATG GTT GTG ATG TCC GCC 234
ACG CTC TGC TCT GCC CTC TAC GTG GGG GAC CTC TGC GGC 273
GGG GTG ATG CTC GCA GCC CAG ATG TTC ATT GTC TCG CCG 312
CGA CGC CAC TGG TTT GTG CAA GAA TGC AAT TGC TCC ATC 351
TAC CCC GGT ACC ATC ACT GGA CAC CGT ATG GCA TGG GAC 390
ATG ATG ATG AAC TGG TCG CCC ACA GCC ACC ATG ATC CTG 429
GCG TAC GCG ATG CGC GTT CCC GAG GTC ATC ATA GAC ATC 468
ATC GGC GGG GCT CAC TGG GGC GTC ATG TTT GGC TTG GCC 507
TAC TTC TCT ATG CAG GGA GCG TGG GCG AAG GTC ATT GTC 546
ATC CTC TTG CTG GCT GCT GGG GTG GAC GCG 576

(2) INFORMATION FOR SEQ ID NO:27:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 576 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(vi) ORIGINAL SOURCE:
(A) ORGANISM: homosapiens
(C) INDIVIDUAL ISOLATE: T4

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

GCA CAA GTG AAG AAC ACC ACT AAC AGC TAC ATG GTG ACC 39
AAC GAC TGT TCT AAT GAC AGC ATC ACT TGG CAG CTC CAG 78
GCC GCG GTC CTC CAC GTC CCC GGG TGT GTC CCG TGC GAG 117

AAA ACG GGA AAT ACA TCT CGG TGC TGG ATA CCG GTT TCA 156
CCA AAC GTG GCC GTG CGG CAG CCC GGC GCC CTC ACG CAG 195
GGC TTG CGG ACG CAC ATT GAC ATG GTT GTG ATG TCC GCC 234
ACG CTC TGC TCT GCT CTT TAC GTG GGG GAC CTC TGC GGC 273
GGG GTG ATG CTC GCA GCC CAG ATG TTC ATC GTC TCG CCG 312
CAA CAT CAC TGG TTT GTG CAA GAC TGC AAT TGC TCT ATC 351
TAC CCT GGC ACC ATC ACT GGA CAC CGT ATG GCA TGG GAT 390
ATG ATG ATG AAC TGG TCG CCC ACG GCC ACC ATG ATC CTG 429
GCG TAC GCG ATG CGC GTT CCC GAG GTC ATC TTA GAC ATC 468
GTT AGC GGG GCA CAC TGG GGC GTC ATG TTC GGC TTG GCC 507
TAC TTC TCT ATG CAG GGA GCG TGG GCG AAA GTC GTT GTC 546
ATC CTT CTG CTG GCC GCT GGG GTG GAC GCG 576

(2) INFORMATION FOR SEQ ID NO:28:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 576 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(vi) ORIGINAL SOURCE:
(A) ORGANISM: homosapiens
(C) INDIVIDUAL ISOLATE: T9

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

GCC GAA GTG AAG AAC ACC AGT ACC AGC TAC ATG GTG ACA 39
AAT GAC TGT TCC AAC GAC AGC ATC ACC TGG CAA CTC CAG 78
GCC GCG GTC CTC CAC GTC CCC GGG TGC GTC CCG TGC GAG 117
AGA GTT GGA AAC GCG TCG CGG TGC TGG ATA CCG GTC TCG 156
CCA AAC GTA GCT GTG CAG CGG CCT GGC GCC CTC ACG CAG 195
GGC TTG CGG ACG CAC ATC GAC ATG GTT GTG ATG TCC GCC 234
ACG CTC TGC TCC GCT CTC TAC GTG GGG GAT CTC TGC GGC 273
GGG GTA ATG CTC GCC GCT CAG ATG TTC ATT ATC TCG CCG 312
CAG CAC CAC TGG TTT GTG CAG GAA TGC AAC TGC TCC ATT 351
TAC CCT GGT ACC ATC ACT GGA CAC CGT ATG GCA TGG GAC 390
ATG ATG ATG AAC TGG TCG CCC ACA ACC ACC ATG ATC TTG 429
GCG TAC GCG ATG CGC GTT CCC GAG GTC ATC ATA GAC ATC 468
ATC AGC GGA GCT CAC TGG GGC GTC ATG TTC GGC CTA GCC 507
TAC TTC TCT ATG CAG GGA GCG TGG GCG AAG GTC GTT GTC 546
ATC CTG TTG CTC ACC GCT GGC GTG GAC GCG 576

(2) INFORMATION FOR SEQ ID NO:29:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 576 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(vi) ORIGINAL SOURCE:

(A) ORGANISM: homosapiens
(C) INDIVIDUAL ISOLATE: 10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

```
GTC CAA GTG AAA AAC ACC AGT ACC AGC TAT ATG GTG ACC      39
AAT GAC TGC TCC AAC GAC AGC ATC ACT TGG CAA CTT GAG      78
GCT GCG GTC CTC CAC GTT CCC GGG TGT GTC CCG TGC GAG     117
AAA GTG GGA AAT ACA TCT CGG TGC TGG ATA CCG GTC TCA     156
CCA AAT GTG GCC GTG CAG CGG CCT GGC GCC CTC ACG CAG     195
GGC TTG CGG ACT CAC ATC GAC ATG GTC GTG ATG TCC GCC     234
ACG CTC TGC TCC GCT CTT TAC GTG GGG GAC TTC TGC GGT     273
GGG ATG ATG CTC GCA GCC CAA ATG TTC ATT GTC TCG CCG     312
CGC CAC CAC TCG TTT GTG CAG GAA TGC AAC TGC TCC ATC     351
TAC CCC GGT ACC ATC ACC GGG CAC CGT ATG GCA TGG GAC     390
ATG ATG ATG AAC TGG TCG CCC ACG GCC ACT TTG ATC CTG     429
GCG TAC GTG ATG CGC GTT CCC GAG GTC ATC ATA GAC ATC     468
ATT AGC GGG GCG CAT TGG GGC GTC TTG TTC GGC TTA GCC     507
TAC TTC TCT ATG CAG GGA GCG TGG GCG AAA GTC GTT GTC     546
ATC CTT CTG CTA GCC GCT GGG GTG GAC GCG                 576
```

(2) INFORMATION FOR SEQ ID NO:30:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 576 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(vi) ORIGINAL SOURCE:
(A) ORGANISM: homosapiens
(C) INDIVIDUAL ISOLATE: DK8

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

```
GTG GAA GTC AGG AAC ATC AGT TCC AGC TAC TAC GCC ACC      39
AAT GAT TGC TCA AAC AAC AGC ATC ACC TGG CAA CTC ACC      78
GAC GCA GTT CTC CAC CTT CCC GGA TGC GTC CCA TGT GAG     117
AAT GAC AAT GGC ACC CTG CGC TGC TGG ATA CAA GTG ACA     156
CCT AAT GTG GCT GTG AAA CAC CGC GGC GCA CTT ACT CAT     195
AAC CTG CGA ACA CAC GTC GAC GTG ATC GTA ATG GCA GCT     234
ACG GTC TGC TCG GCC TTG TAT GTG GGA GAC GTA TGC GGG     273
GCC GTG ATG ATC GTG TCG CAG GCT CTC ATA ATA TCG CCT     312
GAA CGC CAC AAC TTT ACC CAG GAG TGC AAC TGT TCC ATC     351
TAC CAA GGT CAT ATC ACC GGC CAC CGC ATG GCA TGG GAC     390
ATG ATG CTA AAC TGG TCA CCA ACT CTT ACC ATG ATC CTC     429
GCC TAT GCC GCT CGT GTT CCT GAG CTA GCC CTC CAG GTT     468
GTC TTC GGC GGC CAT TGG GGC GTG GTG TTT GGC TTG GCC     507
TAT TTC TCC ATG CAG GGA GCG TGG GCC AAA GTC ATT GCC     546
ATC CTC CTT CTT GTC GCA GGA GTG GAT GCA                 576
```

(2) INFORMATION FOR SEQ ID NO:31:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 576 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(vi) ORIGINAL SOURCE:
(A) ORGANISM: homosapiens
(C) INDIVIDUAL ISOLATE: DK11

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

```
GTG GAA GTC AGG AAC ACC AGT TCT AGT TAC TAC GCC ACC      39
AAT GAT TGC TCA AAC AAC AGC ATC ACC TGG CAA CTC ACC      78
AAC GCA GTT CTC CAC CTT CCC GGA TGC GTC CCA TGT GAG     117
AAT GAC AAT GGC ACC CTG CAC TGC TGG ATA CAA GTG ACA     156
CCT AAT GTG GCT GTG AAA CAC CGC GGC GCA CTC ACT CAC     195
AAC CTG CGA GCA CAT ATA GAT ATG ATT GTA ATG GCA GCT     234
ACG GTC TGC TCG GCC TTG TAT GTG GGA GAC GTG TGC GGG     273
GCC GTG ATG ATC GTG TCG CAG GCT TTC ATA GTA TCG CCA     312
GAA CAC CAC CAC TTT ACC CAA GAG TGC AAC TGT TCC ATC     351
TAC CAA GGT CAC ATC ACC GGC CAC CGC ATG GCA TGG GAC     390
ATG ATG CTT AAC TGG TCA CCA ACT CTC ACC ATG ATC CTC     429
GCC TAT GCC GCC CGT GTT CCT GAG CTA GTC CTT GAA GTC     468
GTC TTC GGT GGT CAT TGG GGT GTG GTG TTT GGC TTG GCC     507
TAT TTC TCC ATG CAG GGA GCG TGG GCC AAG GTC ATT GCC     546
ATC CTC CTT CTT GTA GCA GGA GTG GAT GCA                576
```

(2) INFORMATION FOR SEQ ID NO:32:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 576 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(vi) ORIGINAL SOURCE:
(A) ORGANISM: homosapiens
(C) INDIVIDUAL ISOLATE: SW3

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

```
GTG GAA GTC AGG AAC ATC AGT TCT AGC TAC TAT GCC ACC      39
AAT GAT TGC TCA AAC AGC AGC ATC ACC TGG CAA CTC ACC      78
AAC GCA GTC CTC CAC CTT CCC GGA TGC GTC CCG TGT GAG     117
AAT GAT AAT GGC ACC CTG CAC TGC TGG ATA CAA GTG ACA     156
CCT AAT GTG GCT GTG AAA CAC CGC GGC GCG CTC ACT CAC     195
AAC CTG CGA GCA CAC GTC GAT ATG ATC GTA ATG GCA GCT     234
ACG GTC TGC TCG GCC TTG TAT GTG GGA GAC ATG TGC GGG     273
GCC GTG ATG ATC GTG TCG CAG GCT TTC ATA ATA TCG CCA     312
GAA CGC CAC AAC TTT ACC CAA GAG TGC AAC TGT TCC ATC     351
TAC CAA GGT CGT ATC ACC GGC CAC CGC ATG GCG TGG GAC     390
ATG ATG CTA AAC TGG TCA CCA ACT CTT ACC ATG ATC CTT     429
```

GCC TAT GCC GCT CGT GTT CCT GAG CTA GTC CTT GAA GTT 468
GTC TTC GGC GGC CAT TGG GGC GTG GTG TTT GGC TTG GCC 507
TAT TTC TCC ATG CAA GGA GCG TGG GCC AAG GTC ATT GCC 546
ATC CTC CTG CTT GTC GCA GGA GTG GAT GCA 576

(2) INFORMATION FOR SEQ ID NO:33:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 576 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(vi) ORIGINAL SOURCE:
(A) ORGANISM: homosapiens
(C) INDIVIDUAL ISOLATE: T8

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

GTG GAA GTT AGA AAC ACC AGT TTT AGC TAC TAC GCC ACC 39
AAT GAT TGC TCG AAC AAC AGC ATC ACC TGG CAG CTC ACC 78
AAC GCA GTT CTC CAC CTT CCC GGA TGC GTC CCA TGT GAG 117
AAT GAC AAT GGC ACC TTG CGC TGC TGG ATA CAA GTA ACA 156
CCT AAT GTG GCT GTG AAA CAC CGT GGC GCA CTC ACT CAC 195
AAC CTG CGA ACG CAT GTC GAC GTG ATC GTA ATG GCA GCT 234
ACG GTC TGC TCG GCC TTG TAT GTG GGG GAC GTG TGC GGG 273
GCC GTG ATG ATA GCG TCG CAG GCT TTC ATA ATA TCG CCA 312
GAA CGC CAC AAC TTC ACC CAG GAG TGC AAC TGT TCC ATC 351
TAC CAA GGT CAT ATC ACC GGC CAC CGC ATG GCA TGG GAC 390
ATG ATG CTG AAC TGG TCA CCA ACT CTC ACC ATG ATC CTC 429
GCC TAC GCT GCT CGT GTG CCT GAA CTA GTC CTT GAA GTT 468
GTC TTC GGC GGC CAT TGG GGC GTG GTG TTT GGC TTG GCC 507
TAT TTC TCC ATG CAA GGA GCG TGG GCC AAA GTC ATC GCC 546
ATC CTC CTC CTT GTC GCA GGA GTG GAC GCA 576

(2) INFORMATION FOR SEQ ID NO:34:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 576 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(vi) ORIGINAL SOURCE:
(A) ORGANISM: homosapiens
(C) INDIVIDUAL ISOLATE: S83

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

GTG GAG GTC AAG GAC ACC GGC GAC TCC TAC ATG CCG ACC 39
AAC GAT TGC TCC AAC TCT AGT ATC GTT TGG CAG CTT GAA 78
GGA GCA GTG CTT CAT ACT CCT GGA TGC GTC CCT TGT GAG 117

CGT ACC GCC AAC GTC TCT CGA TGT TGG GTG CCG GTT GCC 156
CCC AAT CTC GCC ATA AGT CAA CCT GGC GCT CTC ACT AAG 195
GGC CTG CGA GCA CAC ATC GAT ATC ATC GTG ATG TCT GCT 234
ACG GTC TGT TCT GCC CTT TAT GTG GGG GAC GTG TGT GGC 273
GCG CTG ATG CTG GCC GCT CAG GTC GTC GTC GTG TCG CCA 312
CAA CAC CAT ACG TTT GTC CAG GAA TGC AAC TGT TCC ATA 351
TAC CCG GGC CGC ATT ACG GGA CAC CGC ATG GCT TGG GAT 390
ATG ATG ATG AAC TGG TCG CCC ACT ACC ACC ATG CTC CTG 429
GCG TAC TTG GTG CGC ATC CCG GAA GTC ATC TTG GAT ATT 468
GTT ACA GGA GGT CAT TGG GGT GTA ATG TTT GGC CTC GCT 507
TAC TTC TCC ATG CAG GGA TCG TGG GCG AAG GTC ATC GTT 546
ATC CTC CTG CTG ACT GCT GGG GTG GAG GCG 576

(2) INFORMATION FOR SEQ ID NO:35:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 576 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(vi) ORIGINAL SOURCE:
(A) ORGANISM: homosapiens
(C) INDIVIDUAL ISOLATE: DK12

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

TTA GAG TGG CGG AAT GTG TCC GGC CTC TAC GTC CTT ACC 39
AAC GAC TGT TCC AAT AGC AGT ATC GTG TAT GAG GCC GAT 78
GAC GTC ATT CTG CAC ACA CCT GGC TGT GTA CCT TGT GTT 117
CAG GAC GGC AAT ACA TCT ACG TGC TGG ACC TCA GTG ACG 156
CCT ACA GTG GCA GTC AGG TAC GTC GGA GCA ACC ACC GCT 195
TCG ATA CGC AGT CAT GTG GAC CTG CTA GTG GGC GCG GCC 234
ACG ATG TGC TCT GCG CTC TAC GTG GGT GAT GTG TGT GGG 273
GCC GTC TTC CTT GTG GGA CAA GCC TTC ACG TTC AGA CCT 312
CGT CGC CAT CAA ACA GTC CAG ACC TGT AAC TGC TCG CTG 351
TAC CCA GGC CAT CTT TCA GGA CAT CGA ATG GCT TGG GAT 390
ATG ATG ATG AAT TGG TCC CCC GCT GTG GGT ATG GTG GTA 429
GCG CAC GTC CTG CGT CTG CCC CAG ACC TTG TTC GAC ATA 468
ATA GCT GGG GCC CAT TGG GGC ATC ATG GCG GGC CTA GCC 507
TAT TAC TCC ATG CAG GGC AAC TGG GCC AAG GTC GCT ATC 546
ATC ATG GTT ATG TTT TCA GGA GTC GAT GCC 576

(2) INFORMATION FOR SEQ ID NO:36:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 576 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(vi) ORIGINAL SOURCE:

(A) ORGANISM: homosapiens
(C) INDIVIDUAL ISOLATE: HK10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

```
CTA GAG TGG CGG AAT GTG TCT GGC CTC TAT GTC CTT ACC      39
AAC GAC TGT CCC AAT AGC AGT ATT GTG TAT GAG GCC GAT      78
GAC GTC ATT CTG CAC ACA CCT GGC TGT GTA CCT TGT GTT     117
CAG GAC GGC AAT ACA TCC ACG TGC TGG ACC TCG GTG ACA     156
CCT ACA GTG GCA GTC AGG TAC GTC GGA GCA ACC ACC GCC     195
TCG ATA CGC AGT CAT GTG GAC CTG TTA GTG GGC GCG GCC     234
ACG ATG TGC TCT GCG CTC TAC GTG GGC GAT ATG TGT GGG     273
GCC GTC TTC CTC GTG GGA CAA GCC TTC ACG TTC AGA CCG     312
CGT CGC CAT CAA ACG GTC CAG ACC TGT AAC TGC TCG CTG     351
TAC CCA GGC CAC CTT TCA GGA CAT CGA ATG GCT TGG GAT     390
ATG ATG ATG AAT TGG TCC CCC GCC GTG GGT ATG GTG GTG     429
GCG CAC GTC CTG CGG TTG CCC CAG ACC TTG TTC GAC ATA     468
ATA GCC GGG GCC CAT TGG GGC ATC TTG GCA GGC CTA GCC     507
TAT TAC TCC ATG CAG GGC AAC TGG GCC AAG GTC GCT ATC     546
ATC ATG GTT ATG TTT TCA GGG GTC GAT GCC                576
```

(2) INFORMATION FOR SEQ ID NO:37:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 576 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(vi) ORIGINAL SOURCE:
(A) ORGANISM: homosapiens
(C) INDIVIDUAL ISOLATE: S2

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

```
CTA GAG TGG CGG AAT ACG TCT GGC CTC TAT GTC CTC ACC      39
AAC GAC TGT TCC AAT AGC AGT ATT GTG TAT GAG GCC GAT      78
GAC GTT ATT CTG CAC ACA CCT GGC TGT GTA CCT TGT GTT     117
CAG GAC GGT AAT ACA TCC ACG TGC TGG ACC CCA GTG ACA     156
CCT ACA GTG GCA GTC AGG TAT GTC GGA GCA ACC ACC GCT     195
TCG ATA CGC AGT CAT GTG GAC CTA TTG GTG GGC GCG GCC     234
ACT ATG TGC TCT GCG CTC TAC GTG GGT GAT ATG TGT GGG     273
GCC GTC TTT CTC GTG GGA CAA GCC TTC ACG TTC AGA CCT     312
CGT CGC CAT CAA ACG GTC CAG ACC TGT AAC TGC TCG CTG     351
TAC CCA GGC CAT CTT TCA GGA CAT CGC ATG GCT TGG GAT     390
ATG ATG ATG AAT TGG TCC CCC GCT GTG GGT ATG GTG GTG     429
GCG CAC GTT CTG CGT TTG CCC CAG ACC GTG TTC GAC ATA     468
ATA GCC GGG GCC CAT TGG GGC ATC TTG GCG GGC CTA GCC     507
TAT TAC TCC ATG CAA GGC AAC TGG GCC AAG GTC GCT ATC     546
ATC ATG GTT ATG TTT TCA GGG GTC GAC GCC                576
```

(2) INFORMATION FOR SEQ ID NO:38:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 576 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(vi) ORIGINAL SOURCE:
(A) ORGANISM: homosapiens
(C) INDIVIDUAL ISOLATE: S52

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

```
CTA GAG TGG CGG AAT ACG TCT GGC CTC TAT GTC CTT ACC      39
AAC GAC TGT TCC AAT AGC AGT ATT GTG TAT GAG GCC GAT      78
GAC GTC ATT CTG CAC ACA CCC GGC TGT GTA CCT TGT GTT     117
CAG GAC GGC AAT ACA TCC ATG TGC TGG ACC CCA GTG ACA     156
CCT ACG GTG GCA GTC AGG TAC GTC GGA GCA ACC ACC GCT     195
TCG ATA CGC AGT CAT GTG GAC CTA TTA GTG GGC GCG GCC     234
ACG CTG TGC TCT GCG CTC TAT GTG GGT GAT ATG TGT GGG     273
GCC GTC TTT CTC GTG GGA CAA GCC TTC ACG TTC AGA CCT     312
CGT CGC CAT CAA ACG GTC CAG ACC TGT AAC TGC TCG CTG     351
TAC CCA GGC CAT GTT TCA GGA CAT CGA ATG GCT TGG GAT     390
ATG ATG ATG AAT TGG TCC CCC GCT GTG GGT ATG GTG GTG     429
GCG CAC ATC CTG CGA TTG CCC CAG ACC TTG TTT GAC ATA     468
CTG GCC GGG GCC CAT TGG GGC ATC TTG GCG GGC CTA GCC     507
TAT TAT TCT ATG CAG GGC AAC TGG GCC AAG GTC GCT ATT     546
GTC ATG ATT ATG TTT TCA GGG GTC GAT GCC                576
```

(2) INFORMATION FOR SEQ ID NO:39:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 576 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(vi) ORIGINAL SOURCE:
(A) ORGANISM: homosapiens
(C) INDIVIDUAL ISOLATE: S54

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

```
CTA GAG TGG CGG AAT ACG TCT GGC CTC TAT ATC CTT ACC      39
AAC GAC TGT TCC AAT AGC AGT ATT GTG TAT GAG GCC GAT      78
GAC GTC ATT CTG CAC ACA CCC GGC TGT GTA CCT TGT GTT     117
CAG GAC GGC AAT ACA TCC ACG TGC TGG ACC CCA GTG ACA     156
CCT ACG GTG GCA GTC AGG TAC GTC GGA GCA ACC ACC GCT     195
TCG ATA CGC AGT CAT GTG GAC CTA TTA GTG GGC GCG GCC     234
ACG CTG TGC TCT GCG CTC TAT GTG GGT GAT ATG TGT GGG     273
GCC GTC TTT CTC GTG GGA CAA GCC TTC ACG TTC AGA CCT     312
CGT CGC CAT CAA ACG GTC CAG ACC TGT AAC TGC TCG CTG     351
TAC CCA GGC CAT CTT TCA GGA CAT CGA ATG GCT TGG GAT     390
ATG ATG ATG AAT TGG TCC CCC GCT GTG GGT ATG GTG GTG     429
```

GCG CAC ATC CTG CGA TTG CCC CAG ACC TTG TTT GAC ATA 468
CTG GCC GGG GCC CAT TGG GGC ATC TTG GCG GGC CTA GCC 507
TAT TAT TCT ATG CAG GGC AAC TGG GCC AAG GTC GCT ATC 546
ATC ATG ATT ATG TTT TCA GGG GTC GAT GCC 576

(2) INFORMATION FOR SEQ ID NO:40:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 576 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(vi) ORIGINAL SOURCE:
(A) ORGANISM: homosapiens
(C) INDIVIDUAL ISOLATE: Z4

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

GAG CAC TAC CGG AAT GCT TCG GGC ATC TAT CAC ATC ACC 39
AAT GAT TGT CCG AAT TCC AGT ATA GTC TAT GAA GCT GAC 78
CAT CAC ATC CTA CAC TTG CCG GGG TGC GTA CCC TGT GTG 117
ATG ACT GGG AAC ACA TCG CGT TGC TGG ACG CCG GTG ACG 156
CCT ACA GTG GCT GTC GCA CAC CCG GGC GCT CCG CTT GAG 195
TCG TTC CGG CGA CAT GTG GAC TTA ATG GTA GGC GCG GCC 234
ACT TTG TGT TCT GCC CTC TAT GTT GGG GAC CTC TGC GGA 273
GGT GCC TTC CTG ATG GGG CAG ATG ATC ACT TTT CGG CCG 312
CGT CGC CAC TGG ACC ACG CAG GAG TGC AAT TGT TCC ATC 351
TAC ACT GGC CAT ATC ACC GGC CAC AGG ATG GCG TGG GAC 390
ATG ATG ATG AAC TGG AGC CCT ACC ACC ACT CTG CTC CTC 429
GCC CAG ATC ATG AGG GTC CCC ACA GCC TTT CTC GAC ATG 468
GTT GCC GGA GGC CAC TGG GGC GTC CTC GCG GGC TTG GCG 507
TAC TTC AGC ATG CAA GGC AAT TGG GCC AAG GTA GTC CTG 546
GTC CTT TTC CTC TTT GCT GGG GTA GAC GCC 576

(2) INFORMATION FOR SEQ ID NO:41:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 576 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(vi) ORIGINAL SOURCE:
(A) ORGANISM: homosapiens
(C) INDIVIDUAL ISOLATE: Z1

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

GTG CAC TAC CGG AAT GCT TCG GGC GTC TAT CAT GTC ACC 39
AAT GAT TGC CCT AAC ACC AGC ATA GTG TAC GAG ACG GAG 78
CAC CAC ATC ATG CAC TTG CCA GGG TGT GTC CCC TGT GTG 117

CGG ACG GAG AAT ACT TCT CGC TGC TGG GTG CCC TTG ACC 156
CCC ACT GTG GCC GCG CCC TAT CCC AAC GCA CCG TTA GAG 195
TCC ATG CGC AGG CAT GTA GAC CTG ATG GTG GGT GCG GCT 234
ACT ATG TGT TCC GCC TTC TAC ATT GGA GAT CTG TGT GGA 273
GGC GTC TTC CTA GTG GGC CAG CTG TTC GAC TTC CGA CCG 312
CGC CGG CAC TGG ACC ACC CAG GAT TGC AAC TGC TCC ATC 351
TAT CCT GGT CAC GTC TCG GGC CAC AGG ATG GCC TGG GAC 390
ATG ATG ATG AAC TGG AGC CCT ACC AGC GCG CTG ATT ATG 429
GCT CAG ATC TTA CGG ATC CCC TCT ATC CTA GGT GAC TTG 468
CTC ACC GGG GGT CAC TGG GGA GTT CTT GCT GGT CTA GCT 507
TTC TTC AGC ATG CAG AGT AAC TGG GCG AAG GTC ATC CTG 546
GTC CTA TTC CTC TTT GCC GGG GTC GAG GGA 576

(2) INFORMATION FOR SEQ ID NO:42:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 576 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(vi) ORIGINAL SOURCE:
(A) ORGANISM: homosapiens
(C) INDIVIDUAL ISOLATE: Z6

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

GTT AAC TAT CGC AAT GCC TCG GGC GTC TAT CAC GTC ACC 39
AAC GAC TGC CCG AAC TCG AGC ATA GTG TAT GAG GCC GAA 78
CAC CAG ATC TTA CAC CTC CCA GGG TGC TTG CCC TGT GTG 117
AGG GTT GGG AAT CAG TCA CGC TGC TGG GTG GCC CTT ACT 156
CCC ACC GTG GCG GTG TCT TAT ATC GGT GCT CCG CTT GAC 195
TCC CTC CGG AGA CAT GTG GAC CTG ATG GTG GGC GCC GCT 234
ACT GTA TGC TCT GCC CTC TAC GTT GGA GAT CTG TGC GGT 273
GGT GCA TTC TTG GTT GGC CAG ATG TTC TCC TTC CAG CCG 312
CGA CGC CAC TGG ACT ACG CAG GAC TGC AAT TGT TCT ATC 351
TAC GCA GGG CAT ATC ACG GGC CAC AGG ATG GCA TGG GAC 390
ATG ATG ATG AAC TGG AGT CCC ACA ACC ACC CTG CTT CTC 429
GCC CAG GTC ATG AGG ATC CCT AGC ACT CTG GTA GAT CTA 468
CTC GCT GGA GGG CAC TGG GGC GTC CTT GTT GGG TTG GCG 507
TAC TTC AGT ATG CAA GCT AAT TGG GCC AAA GTC ATC CTG 546
GTC CTT TTC CTC TTC GCT GGA GTT GAT GCC 576

(2) INFORMATION FOR SEQ ID NO:43:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 576 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(vi) ORIGINAL SOURCE:

(A) ORGANISM: homosapiens
(C) INDIVIDUAL ISOLATE: Z7

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

```
GTC AAC TAT CAC AAT GCC TCG GGC GTC TAT CAC ATC ACC      39
AAC GAC TGC CCG AAC TCG AGC ATA ATG TAT GAG GCC GAA      78
CAC CAC ATC CTA CAC CTC CCA GGG TGC GTA CCC TGT GTG     117
AGG GAG GGG AAC CAG TCA CGC TGC TGG GTG GCC CTT ACT     156
CCC ACC GTG GCG GCG CCT TAT ATC GGT GCA CCG CTT GAA     195
TCC ATC CGG AGA CAT GTG GAC CTG ATG GTA GGC GCT GCT     234
ACA GTG TGC TCC GCT CTC TAC ATT GGG GAC CTG TGC GGT     273
GGC GTA TTT TTG GTT GGT CAG ATG TTT TCT TTC CAG CCG     312
CGA CGC CAC TGG ACT ACG CAG GAC TGC AAT TGT TCC ATC     351
TAT GCG GGG CAC GTT ACA GGC CAC AGA ATG GCA TGG GAC     390
ATG ATG ATG AAC TGG AGT CCC ACA ACC ACC TTG GTC CTC     429
GCC CAG GTT ATG AGG ATC CCT AGC ACT CTG GTG GAC CTA     468
CTC ACT GGA GGG CAC TGG GGT ATC CTT ATC GGG GTG GCA     507
TAC TTC TGC ATG CAA GCT AAT TGG GCC AAG GTC ATT CTG     546
GTC CTT TTC CTC TAC GCT GGA GTT GAT GCC                576
```

(2) INFORMATION FOR SEQ ID NO:44:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 576 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(vi) ORIGINAL SOURCE:
(A) ORGANISM: homosapiens
(C) INDIVIDUAL ISOLATE: DK13

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

```
TAC AAC TAT CGC AAC AGC TCG GGT GTC TAC CAT GTC ACC      39
AAC GAT TGC CCG AAC TCG AGC ATA GTC TAT GAA ACC GAT      78
TAC CAC ATC TTA CAC CTC CCG GGA TGC GTT CCT TGC GTG     117
AGG GAA GGG AAC AAG TCT ACA TGC TGG GTG TCT CTC ACC     156
CCC ACC GTG GCT GCG CAA CAT CTG AAT GCT CCG CTT GAG     195
TCT TTG AGA CGT CAC GTG GAT CTG ATG GTG GGC GGC GCC     234
ACT CTC TGC TCC GCC CTC TAC ATC GGA GAC GTG TGT GGG     273
GGT GTG TTC TTG GTC GGT CAA CTG TTC ACC TTC CAA CCT     312
CGC CGC CAC TGG ACC ACC CAA GAC TGC AAT TGT TCC ATC     351
TAC ACA GGA CAT ATC ACA GGA CAC AGA ATG GCT TGG GAC     390
ATG ATG ATG AAT TGG AGC CCC ACT GCG ACG CTG GTC CTC     429
GCC CAA CTT ATG AGG ATC CCA GGC GCC ATG GTC GAC CTG     468
CTT GCA GGC GGC CAC TGG GGC ATT CTG GTT GGC ATA GCG     507
TAC TTC AGC ATG CAA GCT AAT TGG GCC AAG GTT ATC CTG     546
GTC CTG TTT CTC TTT GCT GGA GTC GAC GCT                576
```

(2) INFORMATION FOR SEQ ID NO:45:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 576 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(vi) ORIGINAL SOURCE:
(A) ORGANISM: homosapiens
(C) INDIVIDUAL ISOLATE: SA1

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

```
GTT CCC TAC CGG AAT GCC TCT GGG GTT TAC CAT GTC ACC      39
AAT GAC TGC CCA AAC TCC TCC ATA GTC TAC GAG GCT GAT      78
AGC CTG ATC TTG CAC GCA CCT GGC TGC GTG CCC TGT GTC     117
AGG CAA GAT AAT GTC AGT AGG TGC TGG GTC CAA ATC ACC     156
CCC ACA CTG TCA GCC CCG ACC TTC GGA GCG GTC ACG GCT     195
CCT CTT CGG AGG GCC GTT GAC TAC TTA GCG GGA GGA GCT     234
GCT CTC TGC TCC GCA CTA TAC GTC GGC GAC GCG TGC GGG     273
GCA GTG TTT CTG GTA GGC CAA ATG TTC ACC TAT AGG CCT     312
CGC CAG CAT ACC ACA GTG CAG GAC TGC AAC TGT TCC ATT     351
TAC AGT GGC CAT ATC ACC GGC CAC CGG ATG GCT TGG GAC     390
ATG ATG ATG AAT TGG TCA CCT ACG ACA GCC TTG CTG ATG     429
GCC CAG ATG CTA CGG ATC CCC CAG GTG GTC ATA GAC ATC     468
ATA GCC GGG GGC CAC TGG GGG GTC TTG TTT GCC GCC GCA     507
TAC TTT GCG TCG GCC GCC AAC TGG GCT AAG GTA GTG CTG     546
GTT CTG TTC CTG TTT GCG GGG GTC GAT GGC                576
```

(2) INFORMATION FOR SEQ ID NO:46:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 576 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(vi) ORIGINAL SOURCE:
(A) ORGANISM: homosapiens
(C) INDIVIDUAL ISOLATE: SA4

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

```
GTT CCC TAC CGA AAC GCC TCT GGG GTT TAT CAT GTC ACC      39
AAT GAT TGC CCA AAC TCT TCC ATA GTT TAC GAG GCT GAT      78
AAC CTG ATC TTG CAT GCA CCT GGT TGC GTG CCT TGT GTC     117
AGG CAA GAT AAT GTC AGT AAG TGC TGG GTC CAA ATC ACC     156
CCC ACG TTG TCA GCC CCG AAT CTC GGA GCG GTC ACG GCT     195
CCT CTT CGG AGG GCC GTT GAC TAC TTA GCG GGA GGG GCT     234
GCC CTC TGC TCC GCA CTA TAC GTC GGG GAC GCG TGC GGG     273
GCA GTG TTT TTG GTA GGC CAA ATG TTC ACC TAT AGG CCT     312
CGC CAG CAC ACT ACG GTG CAA GAC TGC AAT TGC TCT ATT     351
TAC AGT GGC CAT ATC ACC GGC CAC CGG ATG GCA TGG GAC     390
ATG ATG ATG AAT TGG TCA CCT ACG ACG GCC TTG CTG ATG     429
```

GCC CAG TTG CTA CGG ATT CCC CAG GTG GTC ATC GAC ATC 468
ATT GCC GGG GGC CAC TGG GGG GTC TTG TTT GCC GCC GCA 507
TAT TTC GCG TCA GCG GCT AAC TGG GCT AAG GTT ATA CTG 546
GTC TTG TTT CTG TTT GCG GGG GTC GAT GCC 576

(2) INFORMATION FOR SEQ ID NO:47:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 576 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(vi) ORIGINAL SOURCE:
(A) ORGANISM: homosapiens
(C) INDIVIDUAL ISOLATE: SA5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:

GTC CCC TAC CGA AAT GCC TCT GGG GTT TAT CAT GTC ACC 39
AAT GAT TGC CCA AAC TCT TCC ATA GTC TAC GAG GCT GAT 78
AAC CTG ATT CTG CAC GCA CCT GGT TGC GTG CCC TGT GTC 117
AAG GAA GGT AAT GTC AGT AGG TGC TGG GTC CAA ATC ACC 156
CCC ACA TTG TCA GCC CCG AAC CTC GGA GCG GTC ACG GCT 195
CCT CTT CGG AGG GTC GTT GAC TAC TTA GCG GGA GGG GCT 234
GCC CTC TGC TCC GCA CTA TAC GTC GGG GAC GCG TGC GGG 273
GCA GTG TTC TTG GTA GGC CAA ATG TTC ACC TAT AGG CCT 312
CGC CAG CAT ACT ACG GTG CAG GAC TGC AAC TGT TCC ATT 351
TAC AGC GGC CAT ATC ACC GGC CAC CGA ATG GCA TGG GAC 390
ATG ATG ATG AAT TGG TCA CCT ACG ACA GCC TTG GTG ATG 429
GCC CAG GTG CTA CGG ATT CCC CAA GTG GTC ATT GAC ATC 468
ATT GCC GGG GGC CAC TGG GGG GTC TTG TTC GCC GTC GCA 507
TAC TTC GCG TCA GCG GCT AAC TGG GCT AAG GTT GTG CTG 546
GTC CTG TTT CTG TTT GCG GGG GTC GAT GGC 576

(2) INFORMATION FOR SEQ ID NO:48:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 576 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(vi) ORIGINAL SOURCE:
(A) ORGANISM: homosapiens
(C) INDIVIDUAL ISOLATE: SA6

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:

GTT CCT TAC CGG AAT GCC TCT GGG GTG TAT CAT GTT ACC 39
AAT GAT TGC CCA AAC TCT TCC ATA GTC TAT GAG GCT GAT 78
GAC CTG ATC CTA CAC GCA CCT GGC TGC GTG CCC TGT GTC 117
CGG AAG GAT AAT GTC AGT AGA TGC TGG GTT CAT ATC ACC 156

```
CCC ACA CTA TCA GCC CCG AGC CTC GGA GCG GTC ACG GCT      195
CCT CTT CGG AGG GCC GTT GAT TAC TTG GCG GGA GGG GCC      234
GCC CTG TGC TCC GCG TTA TAC GTC GGA GAC GTG TGC GGG      273
GCA TTG TTT TTG GTA GGC CAA ATG TTC ACC TAT AGG CCT      312
CGC CAG CAT GCT ACG GTA CAG GAC TGC AAC TGC TCC ATT      351
TAC AGT GGC CAT ATC ACT GGC CAC CGG ATG GCA TGG GAC      390
ATG ATG ATG AAT TGG TCA CCC GCG ACA GCC TTG GTG ATG      429
GCC CAA ATG CTA CGG ATT CCC CAG GTG GTC ATT GAC ATC      468
ATT GCC GGG GGC CAC TGG GGG GTC TTG TTC GCC GCT GCA      507
TAC TTC GCG TCG GCG GCT AAC TGG GCT AAG GTT GTG CTG      546
GTC TTG TTT CTG TTT GCG GGG GTT GAT GCC                 576
```

(2) INFORMATION FOR SEQ ID NO:49:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 576 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(vi) ORIGINAL SOURCE:
(A) ORGANISM: homosapiens
(C) INDIVIDUAL ISOLATE: SA7

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:

```
GTC CCC TAC CGA AAT GCC TCC GGG GTT TAT CAT GTC ACC       39
AAT GAT TGC CCG AAC TCT TCC ATA GTC TAT GAG GCT GAC       78
AAC CTG ATC CTG CAC GCA CCT GGT TGC GTG CCC TGT GTC      117
AGA CAA AAT AAT GTC AGT AGG TGC TGG GTC CAA ATC ACC      156
CCC ACA TTG TCA GCC CCG AAC CTC GGA GCG GTC ACG GCT      195
CCT CTT CGG AGG GCC GTT GAC TAC CTA GCG GGA GGG GCT      234
GCC CTC TGC TCC GCG CTA TAC GTC GGG GAC GCG TGC GGG      273
GCA GTG TTT TTG GTA GGC CAG ATG TTC AGC TAT AGG CCT      312
CGC CAG CAC ACT ACG GTG CAG GAC TGC AAC TGT TCC ATT      351
TAC AGT GGC CAT ATC ACC GGC CAC CGA ATG GCA TGG GAC      390
ATG ATG ATG AAT TGG TCA CCT ACG ACA GCC TTG GTG ATG      429
GCC CAG TTG CTA CGG ATT CCC CAG GTG GTC ATC GAC ATC      468
ATT GCC GGG GGC CAC TGG GGG GTC TTG TTC GCC GCC GCA      507
TAT TTC GCG TCA GCG GCT AAC TGG GCT AAG GTT GTG CTG      546
GTC TTG TTT CTG TTT GCG GGG GTC GAT GCC                 576
```

(2) INFORMATION FOR SEQ ID NO:50:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 576 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(vi) ORIGINAL SOURCE:
(A) ORGANISM: homosapiens
(C) INDIVIDUAL ISOLATE: SA13

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:

```
GTT CCC TAC CGA AAT GCC TCT GGG GTT TAT CAT GTC ACC      39
AAT GAT TGC CCA AAC TCT TCC ATC GTC TAC GAG GCT GAT      78
GAC CTG ATC TTA CAC GCA CCT GGT TGC GTG CCC TGT GTT     117
AGG CAG GGT AAT GTC AGT AGG TGC TGG GTC CAG ATC ACC     156
CCC ACA CTG TCA GCC CCG AGC CTC GGA GCG GTC ACG GCT     195
CCT CTT CGG AGG GCC GTT GAC TAC TTA GCG GGG GGG GCT     234
GCC CTT TGC TCC GCG TTA TAC GTC GGA GAC GCG TGC GGG     273
GCA GTG TTT TTG GTA GGT CAA ATG TTC ACC TAT AGC CCT     312
CGC CGG CAT AAT GTT GTG CAG GAC TGC AAC TGT TCC ATT     351
TAC AGT GGC CAC ATC ACC GGC CAC CGG ATG GCA TGG GAC     390
ATG ATG ATG AAT TGG TCA CCT ACA ACA GCT TTG GTG ATG     429
GCC CAG TTG TTA CGG ATT CCC CAG GTG GTC ATT GAC ATC     468
ATT GCC GGG GCC CAC TGG GGG GTC TTG TTC GCC GCC GCA     507
TAC TAC GCG TCG GCG GCT AAC TGG GCC AAG GTT GTG CTG     546
GTC CTG TTT CTG TTT GCG GGG GTC GAT GCC                576
```

(2) INFORMATION FOR SEQ ID NO:51:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 576 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(vi) ORIGINAL SOURCE:
(A) ORGANISM: homosapiens
(C) INDIVIDUAL ISOLATE: HK2

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:

```
CTT ACC TAC GGC AAC TCC AGT GGG CTA TAC CAT CTC ACA      39
AAT GAT TGC CCC AAC TCC AGC ATC GTG CTG GAG GCG GAT      78
GCT ATG ATC TTG CAT TTG CCT GGA TGC TTG CCT TGT GTG     117
AGG GTC GAT GAT CGG TCC ACC TGT TGG CAT GCT GTG ACC     156
CCC ACC CTG GCC ATA CCA AAT GCT TCC ACG CCC GCA ACG     195
GGA TTC CGC AGG CAT GTG GAT CTT CTT GCG GGC GCC GCA     234
GTG GTT TGC TCA TCC CTG TAC ATC GGG GAC CTG TGT GGC     273
TCT CTC TTT TTG GCG GGA CAA CTA TTC ACC TTT CAG CCC     312
CGC CGT CAT TGG ACT GTG CAA GAC TGC AAC TGC TCC ATC     351
TAT ACA GGC CAC GTC ACC GGC CAC AGG ATG GCT TGG GAC     390
ATG ATG ATG AAC TGG TCA CCC ACA ACC ACT CTG GTC CTA     429
TCT AGC ATC TTG AGG GTA CCT GAG ATT TGT GCG AGT GTG     468
ATA TTT GGT GGC CAT TGG GGG ATA CTA CTA GCC GTT GCC     507
TAC TTT GGC ATG GCT GGC AAC TGG CTA AAA GTT CTG GCT     546
GTT CTG TTC CTA TTT GCA GGG GTT GAA GCA                576
```

(2) INFORMATION FOR SEQ ID NO:52:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 192 amino acids

(B) TYPE: amino acid
(C) STRANDEDNESS: unknown
(D) TOPOLOGY: unknown

(vi) ORIGINAL SOURCE:
(A) ORGANISM: homosapiens
(C) INDIVIDUAL ISOLATE: DK7

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:

Tyr Gln Val Arg Asn Ser Thr Gly Leu Tyr His Val Thr Asn Asp
5 10 15
Cys Pro Asn Ser Ser Ile Val Tyr Glu Ala Ala Asp Ala Ile Leu
20 25 30
His Thr Pro Gly Cys Val Pro Cys Val Arg Glu Gly Asn Val Ser
35 40 45
Arg Cys Trp Val Ala Met Thr Pro Thr Val Ala Thr Arg Asp Gly
50 55 60
Lys Leu Pro Thr Ala Gln Leu Arg Arg His Ile Asp Leu Leu Val
65 70 75
Gly Ser Ala Thr Leu Cys Ser Ala Leu Tyr Val Gly Asp Leu Cys
80 85 90
Gly Ser Val Phe Leu Val Gly Gln Leu Phe Thr Phe Ser Pro Arg
95 100 105
Arg His Trp Thr Thr Gln Gly Cys Asn Cys Ser Ile Tyr Pro Gly
110 115 120
His Ile Thr Gly His Arg Met Ala Trp Asp Met Met Met Asn Trp
125 130 135
Ser Pro Thr Thr Ala Leu Val Val Ala Gln Leu Leu Arg Ile Pro
140 145 150
Gln Ala Ile Leu Asp Met Ile Ala Gly Ala His Trp Gly Val Leu
155 160 165
Ala Gly Ile Ala Tyr Phe Ser Met Val Gly Asn Trp Ala Lys Val
170 175 180
Leu Val Val Leu Leu Leu Phe Ala Gly Val Asp Ala
185 190

(2) INFORMATION FOR SEQ ID NO:53:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 192 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: unknown
(D) TOPOLOGY: unknown

(vi) ORIGINAL SOURCE:
(A) ORGANISM: homosapiens
(C) INDIVIDUAL ISOLATE: DK9

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:53:

Tyr Gln Val Arg Asn Ser Ser Gly Leu Tyr His Val Thr Asn Asp
5 10 15

Cys Pro Asn Ser Ser Ile Val Tyr Glu Ala Ala Asp Ala Ile Leu
20 25 30
His Ser Pro Gly Cys Val Pro Cys Val Arg Glu Gly Asn Ala Ser
35 40 45
Lys Cys Trp Val Ala Val Ala Pro Thr Val Ala Thr Arg Asp Gly
50 55 60
Lys Leu Pro Ala Thr Gln Leu Arg Arg His Ile Asp Leu Leu Val
65 70 75
Gly Ser Ala Thr Leu Cys Ser Ala Leu Tyr Val Gly Asp Leu Cys
80 85 90
Gly Ser Val Phe Leu Val Gly Gln Leu Phe Thr Phe Ser Pro Arg
95 100 105
Arg His Trp Thr Thr Gln Asp Cys Asn Cys Ser Ile Tyr Pro Gly
110 115 120
His Ile Thr Gly His Arg Met Ala Trp Asp Met Met Met Asn Trp
125 130 135
Ser Pro Thr Ala Ala Leu Val Met Ala Gln Leu Leu Arg Ile Pro
140 145 150
Gln Ala Ile Leu Asp Met Ile Ala Gly Ala His Trp Gly Val Leu
155 160 165
Ala Gly Ile Ala Tyr Phe Ser Met Val Gly Asn Trp Ala Lys Val
170 175 180
Val Val Val Leu Leu Leu Phe Thr Gly Val Asp Ala
185 190

(2) INFORMATION FOR SEQ ID NO:54:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 192 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: unknown
(D) TOPOLOGY: unknown

(vi) ORIGINAL SOURCE:
(A) ORGANISM: homosapiens
(C) INDIVIDUAL ISOLATE: DR1

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:54:

His Gln Val Arg Asn Ser Thr Gly Leu Tyr His Val Thr Asn Asp
5 10 15
Cys Pro Asn Ser Ser Ile Val Tyr Glu Ala Ala Asp Ala Ile Leu
20 25 30
His Ala Pro Gly Cys Val Pro Cys Val Arg Glu Gly Asn Ala Ser
35 40 45
Arg Cys Trp Val Ala Val Thr Pro Thr Val Ala Thr Arg Asp Gly
50 55 60
Lys Leu Pro Thr Thr Gln Leu Arg Arg His Ile Asp Leu Leu Val
65 70 75
Gly Ser Ala Thr Leu Cys Ser Ala Leu Tyr Val Gly Asp Leu Cys
80 85 90
Gly Ser Val Phe Leu Val Gly Gln Leu Phe Thr Phe Ser Pro Arg
95 100 105

```
Arg His Trp Thr Thr Gln Asp Cys Asn Cys Ser Ile Tyr Pro Gly
                110                 115                 120
His Ile Thr Gly His Arg Met Ala Trp Asp Met Met Met Asn Trp
                125                 130                 135
Ser Pro Thr Thr Ala Leu Val Met Ala Gln Leu Leu Arg Ile Pro
                140                 145                 150
Gln Ala Ile Leu Asp Met Ile Ala Gly Ala His Trp Gly Val Leu
                155                 160                 165
Ala Gly Ile Ala Tyr Phe Ser Met Val Gly Asn Trp Ala Lys Val
                170                 175                 180
Val Val Val Leu Leu Leu Phe Ala Gly Val Asp Ala
                185                 190
```

(2) INFORMATION FOR SEQ ID NO:55:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 192 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: unknown
(D) TOPOLOGY: unknown

(vi) ORIGINAL SOURCE:
(A) ORGANISM: homosapiens
(C) INDIVIDUAL ISOLATE: DR4

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:55:

```
His Gln Val Arg Asn Ser Thr Gly Leu Tyr His Val Thr Asn Asp
  5                  10                  15
Cys Pro Asn Ser Ser Ile Val Tyr Glu Ala Ala Asp Ala Ile Leu
                20                  25                  30
His Thr Pro Gly Cys Val Pro Cys Val Arg Glu Gly Asn Thr Ser
                35                  40                  45
Arg Cys Trp Val Ala Val Thr Pro Thr Val Ala Thr Arg Asp Gly
                50                  55                  60
Lys Leu Pro Thr Thr Gln Leu Arg Arg His Ile Asp Leu Leu Val
                65                  70                  75
Gly Ser Ala Thr Leu Cys Ser Ala Leu Tyr Val Gly Asp Leu Cys
                80                  85                  90
Gly Ser Val Phe Leu Val Gly Gln Leu Phe Thr Phe Ser Pro Arg
                95                 100                 105
His His Trp Thr Thr Gln Asp Cys Asn Cys Ser Ile Tyr Pro Gly
               110                 115                 120
His Ile Thr Gly His Arg Met Ala Trp Asp Met Met Met Asn Trp
               125                 130                 135
Ser Pro Thr Thr Ala Leu Val Val Ala Gln Leu Leu Arg Ile Pro
               140                 145                 150
Gln Ala Ile Leu Asp Met Ile Ala Gly Ala His Trp Gly Val Leu
               155                 160                 165
Ala Gly Ile Ala Tyr Phe Ser Met Val Gly Asn Trp Ala Lys Val
               170                 175                 180
Leu Val Val Leu Leu Leu Phe Ala Gly Val Asp Ala
               185                 190
```

(2) INFORMATION FOR SEQ ID NO:56:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 192 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: unknown
(D) TOPOLOGY: unknown

(vi) ORIGINAL SOURCE:
(A) ORGANISM: homosapiens
(C) INDIVIDUAL ISOLATE: S14

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:56:

```
Tyr Gln Val Arg Asn Ser Thr Gly Leu Tyr His Val Thr Asn Asp
 5                  10                  15
Cys Pro Asn Ser Ser Ile Val Tyr Glu Thr Ala Asp Ala Ile Leu
            20                  25                  30
His Ala Pro Gly Cys Val Pro Cys Val Arg Glu Gly Asn Thr Ser
        35                  40                  45
Arg Cys Trp Val Ala Met Thr Pro Thr Val Ala Thr Arg Asp Gly
    50                  55                  60
Lys Leu Pro Ala Thr Gln Leu Arg Arg Tyr Ile Asp Leu Leu Val
65                  70                  75
Gly Ser Ala Thr Leu Cys Ser Ala Leu Tyr Val Gly Asp Leu Cys
            80                  85                  90
Gly Ser Val Phe Leu Val Gly Gln Leu Phe Thr Phe Ser Pro Arg
        95                  100                 105
Arg Leu Trp Thr Thr Gln Asp Cys Asn Cys Ser Ile Tyr Pro Gly
    110                 115                 120
His Ile Thr Gly His Arg Met Ala Trp Asp Met Met Met Asn Trp
125                 130                 135
Ser Pro Thr Thr Ala Leu Val Val Ala Gln Leu Leu Arg Ile Pro
            140                 145                 150
Gln Ala Ile Leu Asp Met Ile Ala Gly Ala His Trp Gly Val Leu
        155                 160                 165
Ala Gly Ile Ala Tyr Phe Ser Met Val Gly Asn Trp Ala Lys Val
    170                 175                 180
Leu Val Val Leu Leu Leu Phe Ala Gly Val Asp Ala
185                 190
```

(2) INFORMATION FOR SEQ ID NO:57:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 192 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: unknown
(D) TOPOLOGY: unknown

(vi) ORIGINAL SOURCE:
(A) ORGANISM: homosapiens
(C) INDIVIDUAL ISOLATE: S18

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:57:

Tyr Gln Val Arg Asn Ser Thr Gly Leu Tyr His Val Thr Asn Asp
5 10 15
Cys Pro Asn Ser Ser Ile Val Tyr Glu Thr Ala Asp Thr Ile Leu
20 25 30
His Ser Pro Gly Cys Val Pro Cys Val Arg Glu Gly Asn Ala Ser
35 40 45
Arg Cys Trp Val Pro Val Ala Pro Thr Val Ala Thr Arg Asp Gly
50 55 60
Lys Leu Pro Ala Thr Gln Leu Arg Arg His Ile Asp Leu Leu Val
65 70 75
Gly Ser Ala Thr Leu Cys Ser Ala Leu Tyr Val Gly Asp Leu Cys
80 85 90
Gly Ser Val Phe Leu Val Ser Gln Leu Phe Thr Ile Ser Pro Arg
95 100 105
Arg His Trp Thr Thr Gln Asp Cys Asn Cys Ser Ile Tyr Pro Gly
110 115 120
His Ile Thr Gly His Arg Met Ala Trp Asp Met Met Met Asn Trp
125 130 135
Ser Pro Thr Thr Ala Leu Val Ile Ala Gln Leu Leu Arg Val Pro
140 145 150
Gln Ala Val Leu Asp Met Ile Ala Gly Ala His Trp Gly Val Leu
155 160 165
Ala Gly Ile Ala Tyr Phe Ser Met Ala Gly Asn Trp Ala Lys Val
170 175 180
Leu Leu Val Leu Leu Leu Phe Ala Gly Val Asp Ala
185 190

(2) INFORMATION FOR SEQ ID NO:58:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 192 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: unknown
(D) TOPOLOGY: unknown

(vi) ORIGINAL SOURCE:
(A) ORGANISM: homosapiens
(C) INDIVIDUAL ISOLATE: SW1

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:58:

Tyr Gln Val Arg Asn Ser Ser Gly Leu Tyr His Val Thr Asn Asp
5 10 15
Cys Pro Asn Ser Ser Ile Val Tyr Glu Thr Ala Asp Ala Ile Leu
20 25 30
His Ser Pro Gly Cys Val Pro Cys Val Arg Glu Asp Gly Ala Pro
35 40 45
Lys Cys Trp Val Ala Val Ala Pro Thr Val Ala Thr Arg Asp Gly
50 55 60
Lys Leu Pro Ala Thr Gln Leu Arg Arg His Ile Asp Leu Leu Val
65 70 75

Gly Ser Ala Thr Leu Cys Ser Ala Leu Tyr Val Gly Asp Leu Cys
80 85 90
Gly Ser Val Phe Leu Val Ser Gln Leu Phe Thr Phe Ser Pro Arg
95 100 105
Arg His Trp Thr Thr Gln Asp Cys Asn Cys Ser Ile Tyr Pro Gly
110 115 120
His Ile Thr Gly His Arg Met Ala Trp Asp Met Met Met Asn Trp
125 130 135
Ser Pro Thr Thr Ala Leu Val Val Ala Gln Leu Leu Arg Ile Pro
140 145 150
Gln Ala Val Leu Asp Met Ile Ala Gly Ala His Trp Gly Val Leu
155 160 165
Ala Gly Ile Ala Tyr Phe Ser Met Val Gly Asn Trp Ala Lys Val
170 175 180
Leu Ile Val Leu Leu Leu Phe Ser Gly Val Asp Ala
185 190

(2) INFORMATION FOR SEQ ID NO:59:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 192 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: unknown
(D) TOPOLOGY: unknown

(vi) ORIGINAL SOURCE:
(A) ORGANISM: homosapiens
(C) INDIVIDUAL ISOLATE: US11

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:59:

Tyr Gln Val Arg Asn Ser Thr Gly Leu Tyr His Val Thr Asn Asp
5 10 15
Cys Pro Asn Ser Ser Ile Val Tyr Glu Ala Ala Asp Ala Ile Leu
20 25 30
His Thr Pro Gly Cys Val Pro Cys Val Arg Glu Gly Asn Ala Ser
35 40 45
Arg Cys Trp Val Ala Met Thr Pro Thr Val Ala Thr Arg Asp Gly
50 55 60
Lys Leu Pro Thr Thr Gln Leu Arg Arg His Ile Asp Leu Leu Val
65 70 75
Gly Ser Ala Thr Leu Cys Ser Ala Leu Tyr Val Gly Asp Leu Cys
80 85 90
Gly Ser Val Phe Leu Val Gly Gln Leu Phe Thr Phe Ser Pro Arg
95 100 105
Arg His Trp Thr Thr Gln Gly Cys Asn Cys Ser Ile Tyr Pro Gly
110 115 120
His Ile Thr Gly His Arg Met Ala Trp Asp Met Met Met Asn Trp
125 130 135
Ser Pro Thr Ala Ala Leu Val Val Ala Gln Leu Leu Arg Ile Pro
140 145 150
Gln Ala Ile Leu Asp Met Ile Ala Gly Ala His Trp Gly Val Leu
155 160 165

Ala Gly Ile Ala Tyr Phe Ser Met Val Gly Asn Trp Ala Lys Val
170 175 180
Leu Val Val Leu Leu Leu Phe Ala Gly Val Asp Ala
185 190

(2) INFORMATION FOR SEQ ID NO:60:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 192 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: unknown
(D) TOPOLOGY: unknown

(vi) ORIGINAL SOURCE:
(A) ORGANISM: homosapiens
(C) INDIVIDUAL ISOLATE: D1

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:60:

Tyr Glu Val Arg Asn Val Ser Gly Val Tyr His Val Thr Asn Asp
5 10 15
Cys Ser Asn Ser Ser Ile Val Tyr Glu Thr Ala Asp Met Ile Met
20 25 30
His Thr Pro Gly Cys Val Pro Cys Val Arg Glu Asp Asn Ser Ser
35 40 45
Arg Cys Trp Val Ala Leu Thr Pro Thr Leu Ala Ala Arg Asn Gly
50 55 60
Asn Val Pro Thr Thr Ala Ile Arg Arg His Val Asp Leu Leu Val
65 70 75
Gly Ala Ala Ala Phe Cys Ser Ala Met Tyr Val Gly Asp Leu Cys
80 85 90
Gly Ser Val Phe Leu Ile Ser Gln Leu Phe Thr Leu Ser Pro Arg
95 100 105
Arg His Glu Thr Val Gln Glu Cys Asn Cys Ser Ile Tyr Pro Gly
110 115 120
His Val Thr Gly His Arg Met Ala Trp Asp Met Met Met Asn Trp
125 130 135
Ser Pro Thr Thr Ala Leu Val Val Ser Gln Leu Leu Arg Ile Pro
140 145 150
Gln Ala Val Met Asp Met Val Ala Gly Ala His Trp Gly Val Leu
155 160 165
Ala Gly Leu Ala Tyr Tyr Ser Met Val Gly Asn Trp Ala Lys Val
170 175 180
Leu Ile Val Met Leu Leu Phe Ala Gly Val Asp Gly
185 190

(2) INFORMATION FOR SEQ ID NO:61:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 192 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: unknown

(D) TOPOLOGY: unknown

(vi) ORIGINAL SOURCE:
(A) ORGANISM: homosapiens
(C) INDIVIDUAL ISOLATE: D3

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:61:

```
Tyr Glu Val Arg Asn Val Ser Gly Val Tyr Gln Val Thr Asn Asp
 5                  10                  15
Cys Ser Asn Ser Ser Ile Val Tyr Glu Thr Ala Asp Met Ile Met
            20                  25                  30
His Thr Pro Gly Cys Val Pro Cys Val Arg Glu Asp Asn Ser Ser
        35                  40                  45
Arg Cys Trp Val Ala Leu Thr Pro Thr Leu Ala Ala Arg Asn Ser
    50                  55                  60
Ser Val Pro Thr Thr Thr Ile Arg Arg His Val Asp Leu Leu Val
65                  70                  75
Gly Ala Ala Ala Phe Cys Ser Ala Met Tyr Val Gly Asp Leu Cys
            80                  85                  90
Gly Ser Val Phe Leu Val Ser Gln Leu Phe Thr Phe Ser Pro Arg
        95                  100                 105
Arg His Glu Thr Val Gln Glu Cys Asn Cys Ser Ile Tyr Pro Gly
    110                 115                 120
His Val Thr Gly His Arg Met Ala Trp Asp Met Met Met Asn Trp
125                 130                 135
Ser Pro Thr Ala Ala Leu Val Val Ser Gln Leu Leu Arg Ile Pro
            140                 145                 150
Gln Ala Val Val Asp Met Val Ala Gly Ala His Trp Gly Val Leu
        155                 160                 165
Ala Gly Leu Ala Tyr Tyr Ser Met Val Gly Asn Trp Ala Lys Val
    170                 175                 180
Leu Ile Val Met Leu Leu Phe Ala Gly Val Asp Gly
185                 190
```

(2) INFORMATION FOR SEQ ID NO:62:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 192 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: unknown
(D) TOPOLOGY: unknown

(vi) ORIGINAL SOURCE:
(A) ORGANISM: homosapiens
(C) INDIVIDUAL ISOLATE: DK1

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:62:

```
Tyr Glu Val Arg Asn Val Ser Gly Val Tyr His Val Thr Asn Asp
 5                  10                  15
Cys Ser Asn Ser Ser Ile Val Tyr Glu Ala Val Asp Val Ile Met
            20                  25                  30
```

His Thr Pro Gly Cys Val Pro Cys Val Arg Glu Asn Asn His Ser
35 40 45
Arg Cys Trp Val Ala Leu Thr Pro Thr Leu Ala Ala Arg Asn Ala
50 55 60
Ser Ile Pro Thr Thr Thr Ile Arg Arg His Val Asp Leu Leu Val
65 70 75
Gly Ala Ala Ala Phe Cys Ser Ala Met Tyr Val Gly Asp Leu Cys
80 85 90
Gly Ser Val Phe Leu Val Ser Gln Leu Phe Thr Phe Ser Pro Arg
95 100 105
Arg His Glu Thr Ala Gln Asp Cys Asn Cys Ser Ile Tyr Pro Gly
110 115 120
His Val Ser Gly His Arg Met Ala Trp Asp Met Met Met Asn Trp
125 130 135
Ser Pro Thr Thr Ala Leu Val Leu Ser Gln Leu Leu Arg Ile Pro
140 145 150
Gln Ala Val Val Asp Met Val Ala Gly Ala His Trp Gly Val Leu
155 160 165
Ala Gly Leu Ala Tyr Tyr Ser Met Ala Gly Asn Trp Ala Lys Val
170 175 180
Leu Ile Val Leu Leu Leu Phe Ala Gly Val Asp Gly
185 190

(2) INFORMATION FOR SEQ ID NO:63:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 192 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: unknown
(D) TOPOLOGY: unknown

(vi) ORIGINAL SOURCE:
(A) ORGANISM: homosapiens
(C) INDIVIDUAL ISOLATE: HK3

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:63:

Tyr Glu Val Arg Asn Val Ser Gly Ile Tyr His Val Thr Asn Asp
5 10 15
Cys Ser Asn Ser Ser Val Val Tyr Glu Thr Ala Asp Met Ile Met
20 25 30
His Thr Pro Gly Cys Val Pro Cys Val Arg Glu Asn Asn Ser Ser
35 40 45
Arg Cys Trp Val Ala Leu Thr Pro Thr Leu Ala Ala Arg Asn Val
50 55 60
Ser Val Pro Thr Thr Thr Ile Arg Arg His Val Asp Leu Leu Val
65 70 75
Gly Ala Ala Ala Phe Cys Ser Ala Met Tyr Val Gly Asp Leu Cys
80 85 90
Gly Ser Val Phe Leu Val Ser Gln Leu Phe Thr Phe Ser Pro Arg
95 100 105
Arg His Glu Thr Val Gln Asp Cys Asn Cys Ser Leu Tyr Pro Gly
110 115 120

```
His Val Ser Gly His Arg Met Ala Trp Asp Met Met Met Asn Trp
                125                 130                 135
Ser Pro Thr Ala Ala Leu Val Val Ser Gln Leu Leu Arg Ile Pro
            140                 145                 150
Gln Ala Val Val Asp Met Val Ala Gly Ala His Trp Gly Val Leu
        155                 160                 165
Ala Gly Leu Ala Tyr Tyr Ser Met Val Gly Asn Trp Ala Lys Val
    170                 175                 180
Leu Ile Val Met Leu Leu Phe Ala Gly Val Asp Gly
185                 190
```

(2) INFORMATION FOR SEQ ID NO:64:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 192 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: unknown
(D) TOPOLOGY: unknown

(vi) ORIGINAL SOURCE:
(A) ORGANISM: homosapiens
(C) INDIVIDUAL ISOLATE: HK4

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:64:

```
His Glu Val His Asn Val Ser Gly Ile Tyr His Val Thr Asn Asp
  5                  10                  15
Cys Ser Asn Ser Ser Ile Val Tyr Glu Ala Ala Asp Met Ile Met
            20                  25                  30
His Thr Pro Gly Cys Val Pro Cys Val Arg Glu Asn Asn Ser Ser
        35                  40                  45
Arg Cys Trp Val Ala Leu Thr Pro Thr Leu Ala Ala Arg Asn Ala
    50                  55                  60
Ser Ile Pro Thr Thr Thr Ile Arg Arg His Val Asp Leu Leu Val
65                  70                  75
Gly Ala Ala Ala Phe Cys Ser Ala Met Tyr Val Gly Asp Leu Cys
            80                  85                  90
Gly Ser Val Phe Leu Val Ser Gln Leu Phe Thr Phe Ser Pro Arg
        95                  100                 105
Arg His Glu Thr Val Gln Asp Cys Asn Cys Ser Ile Tyr Pro Gly
    110                 115                 120
His Val Ser Gly His Arg Met Ala Trp Asp Met Met Met Asn Trp
125                 130                 135
Ser Pro Thr Ala Ala Leu Val Val Ser Gln Leu Leu Arg Leu Pro
            140                 145                 150
Gln Ala Val Met Asp Met Val Ala Gly Ala His Trp Gly Val Leu
        155                 160                 165
Ala Gly Leu Ala Tyr Tyr Ser Met Val Gly Asn Trp Ala Lys Val
    170                 175                 180
Leu Ile Val Met Leu Leu Phe Ala Gly Val Asp Gly
185                 190
```

(2) INFORMATION FOR SEQ ID NO:65:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 192 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: unknown
(D) TOPOLOGY: unknown

(vi) ORIGINAL SOURCE:
(A) ORGANISM: homosapiens
(C) INDIVIDUAL ISOLATE: HK5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:65:

Tyr Glu Val Arg Asn Val Ser Gly Val Tyr His Val Thr Asn Asp
5 10 15
Cys Ser Asn Leu Ser Ile Val Tyr Glu Thr Thr Asp Met Ile Met
20 25 30
His Thr Pro Gly Cys Val Pro Cys Val Arg Glu Asn Asn Ser Ser
35 40 45
Arg Cys Trp Val Ala Leu Ala Pro Thr Leu Ala Ala Arg Asn Ala
50 55 60
Ser Val Pro Thr Thr Ala Ile Arg Arg His Val Asp Leu Leu Val
65 70 75
Gly Ala Ala Ala Phe Cys Ser Ala Met Tyr Val Gly Asp Leu Cys
80 85 90
Gly Ser Val Phe Leu Val Ser Gln Leu Phe Thr Phe Ser Pro Arg
95 100 105
Arg His Glu Thr Val Gln Asp Cys Asn Cys Ser Ile Tyr Pro Gly
110 115 120
His Val Thr Gly His Arg Met Ala Trp Asp Met Met Met Asn Trp
125 130 135
Ser Pro Thr Thr Ala Leu Val Val Ser Gln Leu Leu Arg Ile Pro
140 145 150
Gln Ala Val Val Asp Met Val Ala Gly Ala His Trp Gly Val Leu
155 160 165
Ala Gly Leu Ala Tyr Tyr Ser Met Val Gly Asn Trp Ala Lys Val
170 175 180
Leu Ile Val Met Leu Leu Phe Ala Gly Val Asp Gly
185 190

(2) INFORMATION FOR SEQ ID NO:66:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 192 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: unknown
(D) TOPOLOGY: unknown

(vi) ORIGINAL SOURCE:
(A) ORGANISM: homosapiens
(C) INDIVIDUAL ISOLATE: HK8

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:66:

Tyr Glu Val Arg Asn Val Ser Gly Ile Tyr His Val Thr Asn Asp
5 10 15
Cys Ser Asn Ser Ser Ile Val Tyr Glu Thr Ala Asp Met Ile Met
20 25 30
His Thr Pro Gly Cys Met Pro Cys Val Arg Glu Asn Asn Ser Ser
35 40 45
Arg Cys Trp Val Ala Leu Thr Pro Thr Leu Ala Ala Arg Asn Val
50 55 60
Ser Val Pro Thr Thr Thr Ile Arg Arg His Val Asp Leu Leu Val
65 70 75
Gly Ala Ala Ala Phe Cys Ser Ala Met Tyr Val Gly Asp Leu Cys
80 85 90
Gly Ser Val Phe Leu Val Ser Gln Leu Phe Thr Phe Ser Pro Arg
95 100 105
Arg His Glu Thr Val Gln Asp Cys Asn Cys Ser Ile Tyr Pro Gly
110 115 120
His Val Ser Gly His Arg Met Ala Trp Asp Met Met Met Asn Trp
125 130 135
Ser Pro Thr Thr Ala Leu Val Val Ser Gln Leu Leu Arg Ile Pro
140 145 150
Gln Ala Ile Val Asp Met Val Ala Gly Ala His Trp Gly Val Leu
155 160 165
Ala Gly Leu Ala Tyr Tyr Ser Met Val Gly Asn Trp Ala Lys Val
170 175 180
Leu Ile Val Met Leu Leu Phe Ala Gly Val Asp Gly
185 190

(2) INFORMATION FOR SEQ ID NO:67:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 192 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: unknown
(D) TOPOLOGY: unknown

(vi) ORIGINAL SOURCE:
(A) ORGANISM: homosapiens
(C) INDIVIDUAL ISOLATE: IND5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:67:

Tyr Glu Val Arg Asn Val Ser Gly Val Tyr His Val Thr Asn Asp
5 10 15
Cys Ser Asn Ser Ser Ile Val Tyr Glu Ala Ala Asp Met Ile Met
20 25 30
His Thr Pro Gly Cys Val Pro Cys Val Arg Glu Gly Asn Ser Ser
35 40 45
Arg Cys Trp Val Ala Leu Thr Pro Thr Leu Ala Ala Arg Asn Ala
50 55 60
Ser Val Ser Thr Thr Thr Ile Arg His His Val Asp Leu Leu Val
65 70 75

Gly Ala Ala Ala Phe Cys Ser Ala Met Tyr Val Gly Asp Leu Cys
80 85 90
Gly Ser Val Phe Leu Val Ser Gln Leu Phe Thr Phe Ser Pro Arg
95 100 105
Arg His Glu Thr Val Gln Asp Cys Asn Cys Ser Ile Tyr Pro Gly
110 115 120
His Val Ser Gly His Arg Met Ala Trp Asp Met Met Met Asn Trp
125 130 135
Ser Pro Thr Ala Ala Leu Val Val Ser Gln Leu Leu Arg Ile Pro
140 145 150
Gln Ala Val Val Asp Met Val Ala Gly Ala His Trp Gly Ile Leu
155 160 165
Ala Gly Leu Ala Tyr Tyr Ser Met Val Gly Asn Trp Ala Lys Val
170 175 180
Leu Ile Val Met Leu Leu Phe Ala Gly Val Asp Gly
185 190

(2) INFORMATION FOR SEQ ID NO:68:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 192 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: unknown
(D) TOPOLOGY: unknown

(vi) ORIGINAL SOURCE:
(A) ORGANISM: homosapiens
(C) INDIVIDUAL ISOLATE: IND8

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:68:

Tyr Glu Val Arg Asn Val Ser Gly Val Tyr His Val Thr Asn Asp
5 10 15
Cys Ser Asn Ser Ser Ile Val Tyr Glu Ala Ala Asp Met Ile Met
20 25 30
His Thr Pro Gly Cys Val Pro Cys Val Arg Glu Gly Asn Phe Ser
35 40 45
Ser Cys Trp Val Ala Leu Thr Pro Thr Leu Ala Ala Arg Asn Ala
50 55 60
Ser Val Pro Thr Thr Thr Ile Arg Arg His Val Asp Leu Leu Val
65 70 75
Gly Ala Ala Ala Phe Cys Ser Ala Met Tyr Val Gly Asp Leu Cys
80 85 90
Gly Ser Val Phe Leu Val Ser Gln Leu Phe Thr Phe Ser Pro Arg
95 100 105
Arg His Glu Thr Val Gln Asp Cys Asn Cys Ser Ile Tyr Pro Gly
110 115 120
His Val Ser Gly His Arg Met Ala Trp Asp Met Met Met Asn Trp
125 130 135
Ser Pro Thr Ala Ala Leu Val Val Ser Gln Leu Leu Arg Ile Pro
140 145 150
Gln Ala Val Val Asp Met Val Ala Gly Ala His Trp Gly Ile Leu
155 160 165

Ala Gly Leu Ala Tyr Tyr Ser Met Val Gly Asn Trp Ala Lys Val
170 175 180
Leu Ile Val Met Leu Leu Phe Ala Gly Val Asp Gly
185 190

(2) INFORMATION FOR SEQ ID NO:69:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 192 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: unknown
(D) TOPOLOGY: unknown

(vi) ORIGINAL SOURCE:
(A) ORGANISM: homosapiens
(C) INDIVIDUAL ISOLATE: P10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:69:

Tyr Glu Val Arg Asn Val Ser Gly Val Tyr His Val Thr Asn Asp
5 10 15
Cys Ser Asn Ser Ser Ile Val Tyr Glu Ala Ala Asp Met Ile Met
20 25 30
His Thr Pro Gly Cys Val Pro Cys Val Arg Glu Asn Asn Ser Ser
35 40 45
Arg Cys Trp Val Ala Leu Thr Pro Thr Leu Ala Ala Arg Asn Ser
50 55 60
Ser Val Pro Thr Thr Ala Ile Arg Arg His Val Asp Leu Leu Val
65 70 75
Gly Ala Ala Ala Phe Cys Ser Ala Met Tyr Val Gly Asp Leu Cys
80 85 90
Gly Ser Val Leu Leu Val Ser Gln Leu Phe Thr Phe Ser Pro Arg
95 100 105
Arg His Trp Thr Val Gln Asp Cys Asn Cys Ser Ile Tyr Pro Gly
110 115 120
His Val Ser Gly His Arg Met Ala Trp Asp Met Met Met Asn Trp
125 130 135
Ser Pro Thr Ala Ala Leu Val Val Ser Gln Leu Leu Arg Ile Pro
140 145 150
Gln Ala Ile Leu Asp Val Val Ala Gly Ala His Trp Gly Val Leu
155 160 165
Ala Gly Leu Ala Tyr Tyr Ser Met Val Gly Asn Trp Ala Lys Val
170 175 180
Leu Ile Val Met Leu Leu Phe Ala Gly Val Asp Gly
185 190

(2) INFORMATION FOR SEQ ID NO:70:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 192 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: unknown

(D) TOPOLOGY: unknown

(vi) ORIGINAL SOURCE:
(A) ORGANISM: homosapiens
(C) INDIVIDUAL ISOLATE: S9

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:70:

Tyr Glu Val Arg Asn Val Ser Gly Ala Tyr His Val Thr Asn Asp
5 10 15
Cys Ser Asn Ser Ser Ile Val Tyr Glu Ala Ala Asp Val Ile Met
20 25 30
His Thr Pro Gly Cys Val Pro Cys Val Gln Glu Gly Asn Ser Ser
35 40 45
Gln Cys Trp Val Ala Leu Thr Pro Thr Leu Ala Ala Arg Asn Ala
50 55 60
Thr Val Pro Thr Thr Thr Ile Arg Arg His Val Asp Leu Leu Val
65 70 75
Gly Ala Ala Val Phe Cys Ser Ala Met Tyr Val Gly Asp Leu Cys
80 85 90
Gly Ser Val Phe Leu Ile Ser Gln Leu Phe Thr Ile Ser Pro Arg
95 100 105
Arg His Glu Thr Val Gln Asn Cys Asn Cys Ser Ile Tyr Pro Gly
110 115 120
His Val Thr Gly His Arg Met Ala Trp Asp Met Met Met Asn Trp
125 130 135
Ser Pro Thr Thr Ala Leu Val Val Ser Gln Leu Leu Arg Ile Pro
140 145 150
Gln Ala Val Met Asp Met Val Ala Gly Ala His Trp Gly Val Leu
155 160 165
Ala Gly Leu Ala Tyr Tyr Ser Met Val Gly Asn Trp Ala Lys Val
170 175 180
Leu Ile Val Met Leu Leu Phe Ala Gly Val Asp Gly
185 190

(2) INFORMATION FOR SEQ ID NO:71:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 192 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: unknown
(D) TOPOLOGY: unknown

(vi) ORIGINAL SOURCE:
(A) ORGANISM: homosapiens
(C) INDIVIDUAL ISOLATE: S45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:71:

Tyr Glu Val Arg Asn Val Ser Gly Ala Tyr His Val Thr Asn Asp
5 10 15
Cys Ser Asn Ser Ser Ile Val Tyr Glu Ala Val Asp Val Ile Leu
20 25 30

```
His Thr Pro Gly Cys Val Pro Cys Val Arg Glu Asn Asn Ser Ser
                35                  40                  45
Arg Cys Trp Val Ala Leu Thr Pro Thr Leu Ala Ala Arg Asn Ser
            50                  55                  60
Ser Val Pro Thr Thr Thr Ile Arg Arg His Val Asp Leu Leu Val
        65                  70                  75
Gly Ala Ala Ala Phe Cys Ser Ala Met Tyr Val Gly Asp Leu Cys
    80                  85                  90
Gly Ser Val Phe Leu Val Ser Gln Leu Phe Thr Phe Ser Pro Arg
                95                  100                 105
Arg His Glu Thr Val Gln Asp Cys Asn Cys Ser Ile Tyr Pro Gly
            110                 115                 120
His Val Thr Gly His Arg Met Ala Trp Asp Met Met Met Asn Trp
        125                 130                 135
Ser Pro Thr Ala Ala Leu Val Val Ser Gln Leu Leu Arg Ile Pro
    140                 145                 150
Gln Ala Val Val Asp Met Val Ala Gly Ala His Trp Gly Val Leu
155                 160                 165
Ala Gly Leu Ala Tyr Tyr Ser Met Val Gly Asn Trp Ala Lys Val
            170                 175                 180
Leu Ile Val Met Leu Leu Phe Ala Gly Val Asp Gly
        185                 190
```

(2) INFORMATION FOR SEQ ID NO:72:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 192 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: unknown
(D) TOPOLOGY: unknown

(vi) ORIGINAL SOURCE:
(A) ORGANISM: homosapiens
(C) INDIVIDUAL ISOLATE: SA10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:72:

```
Tyr Glu Val Arg Asn Val Ser Gly Met Tyr His Val Thr Asn Asp
 5                  10                  15
Cys Ser Asn Ser Ser Ile Val Tyr Glu Ala Ala Asp Met Ile Met
            20                  25                  30
His Thr Pro Gly Cys Val Pro Cys Val Arg Glu Asn Asn Ser Ser
        35                  40                  45
Arg Cys Trp Val Ala Leu Thr Pro Thr Leu Ala Ala Arg Asn Ser
    50                  55                  60
Ser Val Pro Thr Thr Thr Ile Arg Arg His Val Asp Leu Leu Val
65                  70                  75
Gly Ala Ala Ala Phe Cys Ser Ala Met Tyr Val Gly Asp Leu Cys
            80                  85                  90
Gly Ser Val Phe Leu Val Ser Gln Leu Phe Thr Phe Ser Pro Arg
        95                  100                 105
Arg Tyr Glu Thr Val Gln Asp Cys Asn Cys Ser Ile Tyr Pro Gly
    110                 115                 120
```

Arg Val Thr Gly His Arg Met Ala Trp Asp Met Met Met Asn Trp
125 130 135
Ser Pro Thr Thr Ala Leu Val Val Ser Gln Leu Leu Arg Ile Pro
140 145 150
Gln Ala Ile Val Asp Met Val Ala Gly Ala His Trp Gly Val Leu
155 160 165
Ala Gly Leu Ala Tyr Tyr Ser Met Val Gly Asn Trp Ala Lys Val
170 175 180
Leu Ile Val Met Leu Leu Phe Ala Gly Val Asp Gly
185 190

(2) INFORMATION FOR SEQ ID NO:73:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 192 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: unknown
(D) TOPOLOGY: unknown

(vi) ORIGINAL SOURCE:
(A) ORGANISM: homosapiens
(C) INDIVIDUAL ISOLATE: SW2

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:73:

Tyr Glu Val Arg Asn Val Ser Gly Val Tyr His Val Thr Asn Asp
5 10 15
Cys Ser Asn Ser Ser Ile Val Tyr Glu Thr Ala Asp Met Ile Met
20 25 30
His Thr Pro Gly Cys Val Pro Cys Val Arg Glu Ala Asn Ser Ser
35 40 45
Arg Cys Trp Val Ala Leu Thr Pro Thr Leu Ala Ala Arg Asn Thr
50 55 60
Ser Val Pro Thr Thr Thr Ile Arg Arg His Val Asp Leu Leu Val
65 70 75
Gly Ala Ala Ala Phe Cys Ser Val Met Tyr Val Gly Asp Leu Cys
80 85 90
Gly Ser Val Phe Leu Val Ser Gln Leu Phe Thr Phe Ser Pro Arg
95 100 105
Arg His Glu Thr Val Gln Asp Cys Asn Cys Ser Ile Tyr Pro Gly
110 115 120
His Val Ser Gly His Arg Met Ala Trp Asp Met Met Met Asn Trp
125 130 135
Ser Pro Thr Ala Ala Leu Val Val Ser Gln Leu Leu Arg Ile Pro
140 145 150
Gln Ala Val Val Asp Met Val Ala Gly Ala His Trp Gly Val Leu
155 160 165
Ala Gly Leu Ala Tyr Tyr Ser Met Val Gly Asn Trp Ala Lys Val
170 175 180
Leu Ile Val Met Leu Leu Phe Ala Gly Val Asp Gly
185 190

(2) INFORMATION FOR SEQ ID NO:74:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 192 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: unknown
(D) TOPOLOGY: unknown

(vi) ORIGINAL SOURCE:
(A) ORGANISM: homosapiens
(C) INDIVIDUAL ISOLATE: T3

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:74:

```
Tyr Glu Val Arg Asn Val Ser Gly Val Tyr Tyr Val Thr Asn Asp
                5                  10                  15
Cys Ser Asn Ser Ser Ile Val Tyr Glu Thr Ala Asp Met Ile Met
            20                  25                  30
His Thr Pro Gly Cys Val Pro Cys Val Arg Glu Ser Asn Ser Ser
        35                  40                  45
Arg Cys Trp Val Ala Leu Thr Pro Thr Leu Ala Ala Arg Asn Ala
    50                  55                  60
Ser Val Pro Thr Lys Thr Ile Arg Arg His Val Asp Leu Leu Val
65                  70                  75
Gly Ala Ala Ala Phe Cys Ser Ala Met Tyr Val Gly Asp Leu Cys
                80                  85                  90
Gly Ser Val Phe Leu Val Ser Gln Leu Phe Thr Phe Ser Pro Arg
            95                  100                 105
Arg His Glu Thr Val Gln Asp Cys Asn Cys Ser Ile Tyr Pro Gly
        110                 115                 120
His Val Thr Gly His Arg Met Ala Trp Asp Met Met Met Asn Trp
    125                 130                 135
Ser Pro Thr Thr Ala Leu Val Val Ser Gln Leu Leu Arg Ile Pro
140                 145                 150
Gln Ala Val Val Asp Met Val Ala Gly Ala His Trp Gly Val Leu
155                 160                 165
Ala Gly Leu Ala Tyr Tyr Ser Met Val Gly Asn Trp Ala Lys Val
            170                 175                 180
Leu Ile Val Leu Leu Leu Phe Ala Gly Val Asp Gly
        185                 190
```

(2) INFORMATION FOR SEQ ID NO:75:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 192 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: unknown
(D) TOPOLOGY: unknown

(vi) ORIGINAL SOURCE:
(A) ORGANISM: homosapiens
(C) INDIVIDUAL ISOLATE: T10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:75:

Tyr Glu Val Arg Asn Val Ser Gly Met Tyr His Val Thr Asn Asp
5 10 15
Cys Ser Asn Ser Ser Ile Val Phe Glu Ala Ala Asp Leu Ile Met
20 25 30
His Thr Pro Gly Cys Val Pro Cys Val Arg Glu Gly Asn Ser Ser
35 40 45
Arg Cys Trp Val Ala Leu Thr Pro Thr Leu Ala Ala Arg Asn Thr
50 55 60
Ser Val Pro Thr Thr Thr Ile Arg Arg His Val Asp Leu Leu Val
65 70 75
Gly Ala Ala Ala Phe Cys Ser Ala Met Tyr Val Gly Asp Leu Cys
80 85 90
Gly Ser Val Phe Leu Val Ser Gln Leu Phe Thr Phe Ser Pro Arg
95 100 105
Arg His Glu Thr Leu Gln Asp Cys Asn Cys Ser Ile Tyr Pro Gly
110 115 120
His Leu Ser Gly His Arg Met Ala Trp Asp Met Met Met Asn Trp
125 130 135
Ser Pro Thr Thr Ala Leu Val Val Ser Gln Leu Leu Arg Ile Pro
140 145 150
Gln Ala Val Met Asp Met Val Thr Gly Ala His Trp Gly Val Leu
155 160 165
Ala Gly Leu Ala Tyr Tyr Ser Met Ala Gly Asn Trp Ala Lys Val
170 175 180
Leu Ile Val Met Leu Leu Phe Ala Gly Val Asp Gly
185 190

(2) INFORMATION FOR SEQ ID NO:76:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 192 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: unknown
(D) TOPOLOGY: unknown

(vi) ORIGINAL SOURCE:
(A) ORGANISM: homosapiens
(C) INDIVIDUAL ISOLATE: US6

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:76:

Tyr Glu Val Arg Asn Val Ser Gly Met Tyr His Val Thr Asn Asp
5 10 15
Cys Ser Asn Ser Ser Ile Val Tyr Glu Ala Ala Asp Met Ile Met
20 25 30
His Thr Pro Gly Cys Val Pro Cys Val Arg Glu Asn Asn Ser Ser
35 40 45
Arg Cys Trp Val Ala Leu Thr Pro Thr Leu Ala Ala Arg Asn Ala
50 55 60
Ser Val Pro Thr Thr Thr Ile Arg Arg His Val Asp Leu Leu Val
65 70 75

Gly Ala Ala Thr Phe Cys Ser Ala Met Tyr Val Gly Asp Leu Cys
80 85 90
Gly Ser Val Phe Leu Ile Ser Gln Leu Phe Thr Phe Ser Pro Arg
95 100 105
Gln His Glu Thr Val Gln Asp Cys Asn Cys Ser Ile Tyr Pro Gly
110 115 120
His Val Ser Gly His Arg Met Ala Trp Asp Met Met Met Asn Trp
125 130 135
Ser Pro Thr Ala Ala Leu Val Val Ser Gln Leu Leu Arg Ile Pro
140 145 150
Gln Ala Val Met Asp Met Val Ala Gly Ala His Trp Gly Val Leu
155 160 165
Ala Gly Leu Ala Tyr Tyr Ser Met Val Gly Asn Trp Ala Lys Val
170 175 180
Leu Ile Val Leu Leu Leu Phe Ala Gly Val Asp Gly
185 190

(2) INFORMATION FOR SEQ ID NO:77:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 192 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: unknown
(D) TOPOLOGY: unknown

(vi) ORIGINAL SOURCE:
(A) ORGANISM: homosapiens
(C) INDIVIDUAL ISOLATE: T2

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:77:

Ala Gln Val Arg Asn Thr Ser Arg Gly Tyr Met Val Thr Asn Asp
5 10 15
Cys Ser Asn Glu Ser Ile Thr Trp Gln Leu Gln Ala Ala Val Leu
20 25 30
His Val Pro Gly Cys Ile Pro Cys Glu Arg Leu Gly Asn Thr Ser
35 40 45
Arg Cys Trp Ile Pro Val Thr Pro Asn Val Ala Val Arg Gln Pro
50 55 60
Gly Ala Leu Thr Gln Gly Leu Arg Thr His Ile Asp Met Val Val
65 70 75
Met Ser Ala Thr Leu Cys Ser Ala Leu Tyr Val Gly Asp Leu Cys
80 85 90
Gly Gly Val Met Leu Ala Ala Gln Met Phe Ile Val Ser Pro Arg
95 100 105
Arg His Trp Phe Val Gln Glu Cys Asn Cys Ser Ile Tyr Pro Gly
110 115 120
Thr Ile Thr Gly His Arg Met Ala Trp Asp Met Met Met Asn Trp
125 130 135
Ser Pro Thr Ala Thr Met Ile Leu Ala Tyr Ala Met Arg Val Pro
140 145 150
Glu Val Ile Ile Asp Ile Ile Gly Gly Ala His Trp Gly Val Met
155 160 165

Phe Gly Leu Ala Tyr Phe Ser Met Gln Gly Ala Trp Ala Lys Val
170 175 180
Ile Val Ile Leu Leu Leu Ala Ala Gly Val Asp Ala
185 190

(2) INFORMATION FOR SEQ ID NO:78:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 192 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: unknown
(D) TOPOLOGY: unknown

(vi) ORIGINAL SOURCE:
(A) ORGANISM: homosapiens
(C) INDIVIDUAL ISOLATE: T4

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:78:

Ala Gln Val Lys Asn Thr Thr Asn Ser Tyr Met Val Thr Asn Asp
5 10 15
Cys Ser Asn Asp Ser Ile Thr Trp Gln Leu Gln Ala Ala Val Leu
20 25 30
His Val Pro Gly Cys Val Pro Cys Glu Lys Thr Gly Asn Thr Ser
35 40 45
Arg Cys Trp Ile Pro Val Ser Pro Asn Val Ala Val Arg Gln Pro
50 55 60
Gly Ala Leu Thr Gln Gly Leu Arg Thr His Ile Asp Met Val Val
65 70 75
Met Ser Ala Thr Leu Cys Ser Ala Leu Tyr Val Gly Asp Leu Cys
80 85 90
Gly Gly Val Met Leu Ala Ala Gln Met Phe Ile Val Ser Pro Gln
95 100 105
His His Trp Phe Val Gln Asp Cys Asn Cys Ser Ile Tyr Pro Gly
110 115 120
Thr Ile Thr Gly His Arg Met Ala Trp Asp Met Met Met Asn Trp
125 130 135
Ser Pro Thr Ala Thr Met Ile Leu Ala Tyr Ala Met Arg Val Pro
140 145 150
Glu Val Ile Leu Asp Ile Val Ser Gly Ala His Trp Gly Val Met
155 160 165
Phe Gly Leu Ala Tyr Phe Ser Met Gln Gly Ala Trp Ala Lys Val
170 175 180
Val Val Ile Leu Leu Leu Ala Ala Gly Val Asp Ala
185 190

(2) INFORMATION FOR SEQ ID NO:79:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 192 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: unknown

(D) TOPOLOGY: unknown

(vi) ORIGINAL SOURCE:
(A) ORGANISM: homosapiens
(C) INDIVIDUAL ISOLATE: T9

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:79:

Ala Glu Val Lys Asn Thr Ser Thr Ser Tyr Met Val Thr Asn Asp
5 10 15
Cys Ser Asn Asp Ser Ile Thr Trp Gln Leu Gln Ala Ala Val Leu
20 25 30
His Val Pro Gly Cys Val Pro Cys Glu Arg Val Gly Asn Ala Ser
35 40 45
Arg Cys Trp Ile Pro Val Ser Pro Asn Val Ala Val Gln Arg Pro
50 55 60
Gly Ala Leu Thr Gln Gly Leu Arg Thr His Ile Asp Met Val Val
65 70 75
Met Ser Ala Thr Leu Cys Ser Ala Leu Tyr Val Gly Asp Leu Cys
80 85 90
Gly Gly Val Met Leu Ala Ala Gln Met Phe Ile Ile Ser Pro Gln
95 100 105
His His Trp Phe Val Gln Glu Cys Asn Cys Ser Ile Tyr Pro Gly
110 115 120
Thr Ile Thr Gly His Arg Met Ala Trp Asp Met Met Met Asn Trp
125 130 135
Ser Pro Thr Thr Thr Met Ile Leu Ala Tyr Ala Met Arg Val Pro
140 145 150
Glu Val Ile Ile Asp Ile Ile Ser Gly Ala His Trp Gly Val Met
155 160 165
Phe Gly Leu Ala Tyr Phe Ser Met Gln Gly Ala Trp Ala Lys Val
170 175 180
Val Val Ile Leu Leu Leu Thr Ala Gly Val Asp Ala
185 190

(2) INFORMATION FOR SEQ ID NO:80:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 192 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: unknown
(D) TOPOLOGY: unknown

(vi) ORIGINAL SOURCE:
(A) ORGANISM: homosapiens
(C) INDIVIDUAL ISOLATE: US10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:80:

Val Gln Val Lys Asn Thr Ser Thr Ser Tyr Met Val Thr Asn Asp
5 10 15
Cys Ser Asn Asp Ser Ile Thr Trp Gln Leu Glu Ala Ala Val Leu
20 25 30

His Val Pro Gly Cys Val Pro Cys Glu Lys Val Gly Asn Thr Ser
35 40 45
Arg Cys Trp Ile Pro Val Ser Pro Asn Val Ala Val Gln Arg Pro
50 55 60
Gly Ala Leu Thr Gln Gly Leu Arg Thr His Ile Asp Met Val Val
65 70 75
Met Ser Ala Thr Leu Cys Ser Ala Leu Tyr Val Gly Asp Phe Cys
80 85 90
Gly Gly Met Met Leu Ala Ala Gln Met Phe Ile Val Ser Pro Arg
95 100 105
His His Ser Phe Val Gln Glu Cys Asn Cys Ser Ile Tyr Pro Gly
110 115 120
Thr Ile Thr Gly His Arg Met Ala Trp Asp Met Met Met Asn Trp
125 130 135
Ser Pro Thr Ala Thr Leu Ile Leu Ala Tyr Val Met Arg Val Pro
140 145 150
Glu Val Ile Ile Asp Ile Ile Ser Gly Ala His Trp Gly Val Leu
155 160 165
Phe Gly Leu Ala Tyr Phe Ser Met Gln Gly Ala Trp Ala Lys Val
170 175 180
Val Val Ile Leu Leu Leu Ala Ala Gly Val Asp Ala
185 190

(2) INFORMATION FOR SEQ ID NO:81:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 192 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: unknown
(D) TOPOLOGY: unknown

(vi) ORIGINAL SOURCE:
(A) ORGANISM: homosapiens
(C) INDIVIDUAL ISOLATE: DK8

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:81:

Val Glu Val Arg Asn Ile Ser Ser Ser Tyr Tyr Ala Thr Asn Asp
5 10 15
Cys Ser Asn Asn Ser Ile Thr Trp Gln Leu Thr Asp Ala Val Leu
20 25 30
His Leu Pro Gly Cys Val Pro Cys Glu Asn Asp Asn Gly Thr Leu
35 40 45
Arg Cys Trp Ile Gln Val Thr Pro Asn Val Ala Val Lys His Arg
50 55 60
Gly Ala Leu Thr His Asn Leu Arg Thr His Val Asp Val Ile Val
65 70 75
Met Ala Ala Thr Val Cys Ser Ala Leu Tyr Val Gly Asp Val Cys
80 85 90
Gly Ala Val Met Ile Val Ser Gln Ala Leu Ile Ile Ser Pro Glu
95 100 105
Arg His Asn Phe Thr Gln Glu Cys Asn Cys Ser Ile Tyr Gln Gly
110 115 120

```
His Ile Thr Gly His Arg Met Ala Trp Asp Met Met Leu Asn Trp
                125                 130                 135
Ser Pro Thr Leu Thr Met Ile Leu Ala Tyr Ala Ala Arg Val Pro
            140                 145                 150
Glu Leu Ala Leu Gln Val Val Phe Gly Gly His Trp Gly Val Val
        155                 160                 165
Phe Gly Leu Ala Tyr Phe Ser Met Gln Gly Ala Trp Ala Lys Val
    170                 175                 180
Ile Ala Ile Leu Leu Leu Val Ala Gly Val Asp Ala
185                 190
```

(2) INFORMATION FOR SEQ ID NO:82:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 192 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: unknown
(D) TOPOLOGY: unknown

(vi) ORIGINAL SOURCE:
(A) ORGANISM: homosapiens
(C) INDIVIDUAL ISOLATE: DK11

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:82:

```
Val Glu Val Arg Asn Thr Ser Ser Ser Tyr Tyr Ala Thr Asn Asp
  5                  10                  15
Cys Ser Asn Asn Ser Ile Thr Trp Gln Leu Thr Asn Ala Val Leu
            20                  25                  30
His Leu Pro Gly Cys Val Pro Cys Glu Asn Asp Asn Gly Thr Leu
        35                  40                  45
His Cys Trp Ile Gln Val Thr Pro Asn Val Ala Val Lys His Arg
    50                  55                  60
Gly Ala Leu Thr His Asn Leu Arg Ala His Ile Asp Met Ile Val
65                  70                  75
Met Ala Ala Thr Val Cys Ser Ala Leu Tyr Val Gly Asp Val Cys
                80                  85                  90
Gly Ala Val Met Ile Val Ser Gln Ala Phe Ile Val Ser Pro Glu
            95                  100                 105
His His His Phe Thr Gln Glu Cys Asn Cys Ser Ile Tyr Gln Gly
        110                 115                 120
His Ile Thr Gly His Arg Met Ala Trp Asp Met Met Leu Asn Trp
    125                 130                 135
Ser Pro Thr Leu Thr Met Ile Leu Ala Tyr Ala Ala Arg Val Pro
140                 145                 150
Glu Leu Val Leu Glu Val Val Phe Gly Gly His Trp Gly Val Val
            155                 160                 165
Phe Gly Leu Ala Tyr Phe Ser Met Gln Gly Ala Trp Ala Lys Val
        170                 175                 180
Ile Ala Ile Leu Leu Leu Val Ala Gly Val Asp Ala
    185                 190
```

(2) INFORMATION FOR SEQ ID NO:83:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 192 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: unknown
(D) TOPOLOGY: unknown

(vi) ORIGINAL SOURCE:
(A) ORGANISM: homosapiens
(C) INDIVIDUAL ISOLATE: SW3

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:83:

```
Val Glu Val Arg Asn Ile Ser Ser Ser Tyr Tyr Ala Thr Asn Asp
 5                  10                  15
Cys Ser Asn Ser Ser Ile Thr Trp Gln Leu Thr Asn Ala Val Leu
            20                  25                  30
His Leu Pro Gly Cys Val Pro Cys Glu Asn Asp Asn Gly Thr Leu
        35                  40                  45
His Cys Trp Ile Gln Val Thr Pro Asn Val Ala Val Lys His Arg
    50                  55                  60
Gly Ala Leu Thr His Asn Leu Arg Ala His Val Asp Met Ile Val
65                  70                  75
Met Ala Ala Thr Val Cys Ser Ala Leu Tyr Val Gly Asp Met Cys
                80                  85                  90
Gly Ala Val Met Ile Val Ser Gln Ala Phe Ile Ile Ser Pro Glu
            95                  100                 105
Arg His Asn Phe Thr Gln Glu Cys Asn Cys Ser Ile Tyr Gln Gly
        110                 115                 120
Arg Ile Thr Gly His Arg Met Ala Trp Asp Met Met Leu Asn Trp
    125                 130                 135
Ser Pro Thr Leu Thr Met Ile Leu Ala Tyr Ala Ala Arg Val Pro
140                 145                 150
Glu Leu Val Leu Glu Val Val Phe Gly Gly His Trp Gly Val Val
155                 160                 165
Phe Gly Leu Ala Tyr Phe Ser Met Gln Gly Ala Trp Ala Lys Val
            170                 175                 180
Ile Ala Ile Leu Leu Leu Val Ala Gly Val Asp Ala
        185                 190
```

(2) INFORMATION FOR SEQ ID NO:84:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 192 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: unknown
(D) TOPOLOGY: unknown

(vi) ORIGINAL SOURCE:
(A) ORGANISM: homosapiens
(C) INDIVIDUAL ISOLATE: T8

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:84:

Val Glu Val Arg Asn Thr Ser Phe Ser Tyr Tyr Ala Thr Asn Asp
5 10 15
Cys Ser Asn Asn Ser Ile Thr Trp Gln Leu Thr Asn Ala Val Leu
20 25 30
His Leu Pro Gly Cys Val Pro Cys Glu Asn Asp Asn Gly Thr Leu
35 40 45
Arg Cys Trp Ile Gln Val Thr Pro Asn Val Ala Val Lys His Arg
50 55 60
Gly Ala Leu Thr His Asn Leu Arg Thr His Val Asp Val Ile Val
65 70 75
Met Ala Ala Thr Val Cys Ser Ala Leu Tyr Val Gly Asp Val Cys
80 85 90
Gly Ala Val Met Ile Ala Ser Gln Ala Phe Ile Ile Ser Pro Glu
95 100 105
Arg His Asn Phe Thr Gln Glu Cys Asn Cys Ser Ile Tyr Gln Gly
110 115 120
His Ile Thr Gly His Arg Met Ala Trp Asp Met Met Leu Asn Trp
110 115 120
Ser Pro Thr Leu Thr Met Ile Leu Ala Tyr Ala Ala Arg Val Pro
125 130 135
Glu Leu Val Leu Glu Val Val Phe Gly Gly His Trp Gly Val Val
140 145 150
Phe Gly Leu Ala Tyr Phe Ser Met Gln Gly Ala Trp Ala Lys Val
155 160 165
Ile Ala Ile Leu Leu Leu Val Ala Gly Val Asp Ala
170 175

(2) INFORMATION FOR SEQ ID NO:85:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 192 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: unknown
(D) TOPOLOGY: unknown

(vi) ORIGINAL SOURCE:
(A) ORGANISM: homosapiens
(C) INDIVIDUAL ISOLATE: S83

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:85:

Val Glu Val Lys Asp Thr Gly Asp Ser Tyr Met Pro Thr Asn Asp
5 10 15
Cys Ser Asn Ser Ser Ile Val Trp Gln Leu Glu Gly Ala Val Leu
20 25 30
His Thr Pro Gly Cys Val Pro Cys Glu Arg Thr Ala Asn Val Ser
35 40 45
Arg Cys Trp Val Pro Val Ala Pro Asn Leu Ala Ile Ser Gln Pro
50 55 60
Gly Ala Leu Thr Lys Gly Leu Arg Ala His Ile Asp Ile Ile Val
65 70 75

```
Met Ser Ala Thr Val Cys Ser Ala Leu Tyr Val Gly Asp Val Cys
                80                  85                  90
Gly Ala Leu Met Leu Ala Ala Gln Val Val Val Val Ser Pro Gln
                95                 100                 105
His His Thr Phe Val Gln Glu Cys Asn Cys Ser Ile Tyr Pro Gly
               110                 115                 120
Arg Ile Thr Gly His Arg Met Ala Trp Asp Met Met Met Asn Trp
               125                 130                 135
Ser Pro Thr Thr Thr Met Leu Leu Ala Tyr Leu Val Arg Ile Pro
               140                 145                 150
Glu Val Ile Leu Asp Ile Val Thr Gly Gly His Trp Gly Val Met
               155                 160                 165
Phe Gly Leu Ala Tyr Phe Ser Met Gln Gly Ser Trp Ala Lys Val
               170                 175                 180
Ile Val Ile Leu Leu Leu Thr Ala Gly Val Glu Ala
               185                 190
```

(2) INFORMATION FOR SEQ ID NO:86:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 192 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: unknown
(D) TOPOLOGY: unknown

(vi) ORIGINAL SOURCE:
(A) ORGANISM: homosapiens
(C) INDIVIDUAL ISOLATE: DK12

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:86:

```
Leu Glu Trp Arg Asn Val Ser Gly Leu Tyr Val Leu Thr Asn Asp
                5                  10                  15
Cys Ser Asn Ser Ser Ile Val Tyr Glu Ala Asp Asp Val Ile Leu
               20                  25                  30
His Thr Pro Gly Cys Val Pro Cys Val Gln Asp Gly Asn Thr Ser
               35                  40                  45
Thr Cys Trp Thr Ser Val Thr Pro Thr Val Ala Val Arg Tyr Val
               50                  55                  60
Gly Ala Thr Thr Ala Ser Ile Arg Ser His Val Asp Leu Leu Val
               65                  70                  75
Gly Ala Ala Thr Met Cys Ser Ala Leu Tyr Val Gly Asp Val Cys
               80                  85                  90
Gly Ala Val Phe Leu Val Gly Gln Ala Phe Thr Phe Arg Pro Arg
               95                 100                 105
Arg His Gln Thr Val Gln Thr Cys Asn Cys Ser Leu Tyr Pro Gly
              110                 115                 120
His Leu Ser Gly His Arg Met Ala Trp Asp Met Met Met Asn Trp
              125                 130                 135
Ser Pro Ala Val Gly Met Val Val Ala His Val Leu Arg Leu Pro
              140                 145                 150
Gln Thr Leu Phe Asp Ile Ile Ala Gly Ala His Trp Gly Ile Met
              155                 160                 165
```

Ala Gly Leu Ala Tyr Tyr Ser Met Gln Gly Asn Trp Ala Lys Val
170 175 180
Ala Ile Ile Met Val Met Phe Ser Gly Val Asp Ala
185 190

(2) INFORMATION FOR SEQ ID NO:87:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 192 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: unknown
(D) TOPOLOGY: unknown

(vi) ORIGINAL SOURCE:
(A) ORGANISM: homosapiens
(C) INDIVIDUAL ISOLATE: HK10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:87:

Leu Glu Trp Arg Asn Val Ser Gly Leu Tyr Val Leu Thr Asn Asp
5 10 15
Cys Pro Asn Ser Ser Ile Val Tyr Glu Ala Asp Asp Val Ile Leu
20 25 30
His Thr Pro Gly Cys Val Pro Cys Val Gln Asp Gly Asn Thr Ser
35 40 45
Thr Cys Trp Thr Ser Val Thr Pro Thr Val Ala Val Arg Tyr Val
50 55 60
Gly Ala Thr Thr Ala Ser Ile Arg Ser His Val Asp Leu Leu Val
65 70 75
Gly Ala Ala Thr Met Cys Ser Ala Leu Tyr Val Gly Asp Met Cys
80 85 90
Gly Ala Val Phe Leu Val Gly Gln Ala Phe Thr Phe Arg Pro Arg
95 100 105
Arg His Gln Thr Val Gln Thr Cys Asn Cys Ser Leu Tyr Pro Gly
110 115 120
His Leu Ser Gly His Arg Met Ala Trp Asp Met Met Met Asn Trp
125 130 135
Ser Pro Ala Val Gly Met Val Val Ala His Val Leu Arg Leu Pro
140 145 150
Gln Thr Leu Phe Asp Ile Ile Ala Gly Ala His Trp Gly Ile Leu
155 160 165
Ala Gly Leu Ala Tyr Tyr Ser Met Gln Gly Asn Trp Ala Lys Val
170 175 180
Ala Ile Ile Met Val Met Phe Ser Gly Val Asp Ala
185 190

(2) INFORMATION FOR SEQ ID NO:88:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 192 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: unknown

(D) TOPOLOGY: unknown

(vi) ORIGINAL SOURCE:
(A) ORGANISM: homosapiens
(C) INDIVIDUAL ISOLATE: S2

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:88:

Leu Glu Trp Arg Asn Thr Ser Gly Leu Tyr Val Leu Thr Asn Asp
5 10 15
Cys Ser Asn Ser Ser Ile Val Tyr Glu Ala Asp Asp Val Ile Leu
20 25 30
His Thr Pro Gly Cys Val Pro Cys Val Gln Asp Gly Asn Thr Ser
35 40 45
Thr Cys Trp Thr Pro Val Thr Pro Thr Val Ala Val Arg Tyr Val
50 55 60
Gly Ala Thr Thr Ala Ser Ile Arg Ser His Val Asp Leu Leu Val
65 70 75
Gly Ala Ala Thr Met Cys Ser Ala Leu Tyr Val Gly Asp Met Cys
80 85 90
Gly Ala Val Phe Leu Val Gly Gln Ala Phe Thr Phe Arg Pro Arg
95 100 105
Arg His Gln Thr Val Gln Thr Cys Asn Cys Ser Leu Tyr Pro Gly
110 115 120
His Leu Ser Gly His Arg Met Ala Trp Asp Met Met Met Asn Trp
125 130 135
Ser Pro Ala Val Gly Met Val Val Ala His Val Leu Arg Leu Pro
140 145 150
Gln Thr Val Phe Asp Ile Ile Ala Gly Ala His Trp Gly Ile Leu
155 160 165
Ala Gly Leu Ala Tyr Tyr Ser Met Gln Gly Asn Trp Ala Lys Val
170 175 180
Ala Ile Ile Met Val Met Phe Ser Gly Val Asp Ala
185 190

(2) INFORMATION FOR SEQ ID NO:89:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 192 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: unknown
(D) TOPOLOGY: unknown

(vi) ORIGINAL SOURCE:
(A) ORGANISM: homosapiens
(C) INDIVIDUAL ISOLATE: S52

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:89:

Leu Glu Trp Arg Asn Thr Ser Gly Leu Tyr Val Leu Thr Asn Asp
5 10 15
Cys Ser Asn Ser Ser Ile Val Tyr Glu Ala Asp Asp Val Ile Leu
20 25 30

```
His Thr Pro Gly Cys Val Pro Cys Val Gln Asp Gly Asn Thr Ser
                35                  40                  45
Met Cys Trp Thr Pro Val Thr Pro Thr Val Ala Val Arg Tyr Val
            50                  55                  60
Gly Ala Thr Thr Ala Ser Ile Arg Ser His Val Asp Leu Leu Val
        65                  70                  75
Gly Ala Ala Thr Leu Cys Ser Ala Leu Tyr Val Gly Asp Met Cys
    80                  85                  90
Gly Ala Val Phe Leu Val Gly Gln Ala Phe Thr Phe Arg Pro Arg
                95                  100                 105
Arg His Gln Thr Val Gln Thr Cys Asn Cys Ser Leu Tyr Pro Gly
            110                 115                 120
His Val Ser Gly His Arg Met Ala Trp Asp Met Met Met Asn Trp
        125                 130                 135
Ser Pro Ala Val Gly Met Val Val Ala His Ile Leu Arg Leu Pro
    140                 145                 150
Gln Thr Leu Phe Asp Ile Leu Ala Gly Ala His Trp Gly Ile Leu
155                 160                 165
Ala Gly Leu Ala Tyr Tyr Ser Met Gln Gly Asn Trp Ala Lys Val
            170                 175                 180
Ala Ile Val Met Ile Met Phe Ser Gly Val Asp Ala
        185                 190
```

(2) INFORMATION FOR SEQ ID NO:90:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 192 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: unknown
(D) TOPOLOGY: unknown

(vi) ORIGINAL SOURCE:
(A) ORGANISM: homosapiens
(C) INDIVIDUAL ISOLATE: S54

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:90:

```
Leu Glu Trp Arg Asn Thr Ser Gly Leu Tyr Ile Leu Thr Asn Asp
 5                  10                  15
Cys Ser Asn Ser Ser Ile Val Tyr Glu Ala Asp Asp Val Ile Leu
            20                  25                  30
His Thr Pro Gly Cys Val Pro Cys Val Gln Asp Gly Asn Thr Ser
        35                  40                  45
Thr Cys Trp Thr Pro Val Thr Pro Thr Val Ala Val Arg Tyr Val
    50                  55                  60
Gly Ala Thr Thr Ala Ser Ile Arg Ser His Val Asp Leu Leu Val
65                  70                  75
Gly Ala Ala Thr Leu Cys Ser Ala Leu Tyr Val Gly Asp Met Cys
            80                  85                  90
Gly Ala Val Phe Leu Val Gly Gln Ala Phe Thr Phe Arg Pro Arg
        95                  100                 105
Arg His Gln Thr Val Gln Thr Cys Asn Cys Ser Leu Tyr Pro Gly
    110                 115                 120
```

His Leu Ser Gly His Arg Met Ala Trp Asp Met Met Met Asn Trp
125 130 135
Ser Pro Ala Val Gly Met Val Val Ala His Ile Leu Arg Leu Pro
140 145 150
Gln Thr Leu Phe Asp Ile Leu Ala Gly Ala His Trp Gly Ile Leu
155 160 165
Ala Gly Leu Ala Tyr Tyr Ser Met Gln Gly Asn Trp Ala Lys Val
170 175 180
Ala Ile Ile Met Ile Met Phe Ser Gly Val Asp Ala
185 190

(2) INFORMATION FOR SEQ ID NO:91:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 192 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: unknown
(D) TOPOLOGY: unknown

(vi) ORIGINAL SOURCE:
(A) ORGANISM: homosapiens
(C) INDIVIDUAL ISOLATE: Z4

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:91:

Glu His Tyr Arg Asn Ala Ser Gly Ile Tyr His Ile Thr Asn Asp
5 10 15
Cys Pro Asn Ser Ser Ile Val Tyr Glu Ala Asp His His Ile Leu
20 25 30
His Leu Pro Gly Cys Val Pro Cys Val Met Thr Gly Asn Thr Ser
35 40 45
Arg Cys Trp Thr Pro Val Thr Pro Thr Val Ala Val Ala His Pro
50 55 60
Gly Ala Pro Leu Glu Ser Phe Arg Arg His Val Asp Leu Met Val
65 70 75
Gly Ala Ala Thr Leu Cys Ser Ala Leu Tyr Val Gly Asp Leu Cys
80 85 90
Gly Gly Ala Phe Leu Met Gly Gln Met Ile Thr Phe Arg Pro Arg
95 100 105
Arg His Trp Thr Thr Gln Glu Cys Asn Cys Ser Ile Tyr Thr Gly
110 115 120
His Ile Thr Gly His Arg Met Ala Trp Asp Met Met Met Asn Trp
125 130 135
Ser Pro Thr Thr Thr Leu Leu Leu Ala Gln Ile Met Arg Val Pro
140 145 150
Thr Ala Phe Leu Asp Met Val Ala Gly Gly His Trp Gly Val Leu
155 160 165
Ala Gly Leu Ala Tyr Phe Ser Met Gln Gly Asn Trp Ala Lys Val
170 175 180
Val Leu Val Leu Phe Leu Phe Ala Gly Val Asp Ala
185 190

(2) INFORMATION FOR SEQ ID NO:92:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 192 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: unknown
(D) TOPOLOGY: unknown

(vi) ORIGINAL SOURCE:
(A) ORGANISM: homosapiens
(C) INDIVIDUAL ISOLATE: Z1

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:92:

```
Val His Tyr Arg Asn Ala Ser Gly Val Tyr His Val Thr Asn Asp
 5                  10                  15
Cys Pro Asn Thr Ser Ile Val Tyr Glu Thr Glu His His Ile Met
            20                  25                  30
His Leu Pro Gly Cys Val Pro Cys Val Arg Thr Glu Asn Thr Ser
        35                  40                  45
Arg Cys Trp Val Pro Leu Thr Pro Thr Val Ala Ala Pro Tyr Pro
    50                  55                  60
Asn Ala Pro Leu Glu Ser Met Arg Arg His Val Asp Leu Met Val
65                  70                  75
Gly Ala Ala Thr Met Cys Ser Ala Phe Tyr Ile Gly Asp Leu Cys
                80                  85                  90
Gly Gly Val Phe Leu Val Gly Gln Leu Phe Asp Phe Arg Pro Arg
            95                  100                 105
Arg His Trp Thr Thr Gln Asp Cys Asn Cys Ser Ile Tyr Pro Gly
        110                 115                 120
His Val Ser Gly His Arg Met Ala Trp Asp Met Met Met Asn Trp
    125                 130                 135
Ser Pro Thr Ser Ala Leu Ile Met Ala Gln Ile Leu Arg Ile Pro
140                 145                 150
Ser Ile Leu Gly Asp Leu Leu Thr Gly Gly His Trp Gly Val Leu
155                 160                 165
Ala Gly Leu Ala Phe Phe Ser Met Gln Ser Asn Trp Ala Lys Val
            170                 175                 180
Ile Leu Val Leu Phe Leu Phe Ala Gly Val Glu Gly
        185                 190
```

(2) INFORMATION FOR SEQ ID NO:93:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 192 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: unknown
(D) TOPOLOGY: unknown

(vi) ORIGINAL SOURCE:
(A) ORGANISM: homosapiens
(C) INDIVIDUAL ISOLATE: Z6

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:93:

Val Asn Tyr Arg Asn Ala Ser Gly Val Tyr His Val Thr Asn Asp
5 10 15
Cys Pro Asn Ser Ser Ile Val Tyr Glu Ala Glu His Gln Ile Leu
20 25 30
His Leu Pro Gly Cys Leu Pro Cys Val Arg Val Gly Asn Gln Ser
35 40 45
Arg Cys Trp Val Ala Leu Thr Pro Thr Val Ala Val Ser Tyr Ile
50 55 60
Gly Ala Pro Leu Asp Ser Leu Arg Arg His Val Asp Leu Met Val
65 70 75
Gly Ala Ala Thr Val Cys Ser Ala Leu Tyr Val Gly Asp Leu Cys
80 85 90
Gly Gly Ala Phe Leu Val Gly Gln Met Phe Ser Phe Gln Pro Arg
95 100 105
Arg His Trp Thr Thr Gln Asp Cys Asn Cys Ser Ile Tyr Ala Gly
110 115 120
His Ile Thr Gly His Arg Met Ala Trp Asp Met Met Met Asn Trp
125 130 135
Ser Pro Thr Thr Thr Leu Leu Leu Ala Gln Val Met Arg Ile Pro
140 145 150
Ser Thr Leu Val Asp Leu Leu Ala Gly Gly His Trp Gly Val Leu
155 160 165
Val Gly Leu Ala Tyr Phe Ser Met Gln Ala Asn Trp Ala Lys Val
170 175 180
Ile Leu Val Leu Phe Leu Phe Ala Gly Val Asp Ala
185 190

(2) INFORMATION FOR SEQ ID NO:94:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 192 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: unknown
(D) TOPOLOGY: unknown

(vi) ORIGINAL SOURCE:
(A) ORGANISM: homosapiens
(C) INDIVIDUAL ISOLATE: Z7

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:94:

Val Asn Tyr His Asn Ala Ser Gly Val Tyr His Ile Thr Asn Asp
5 10 15
Cys Pro Asn Ser Ser Ile Met Tyr Glu Ala Glu His His Ile Leu
20 25 30
His Leu Pro Gly Cys Val Pro Cys Val Arg Glu Gly Asn Gln Ser
35 40 45
Arg Cys Trp Val Ala Leu Thr Pro Thr Val Ala Ala Pro Tyr Ile
50 55 60
Gly Ala Pro Leu Glu Ser Ile Arg Arg His Val Asp Leu Met Val
65 70 75

Gly Ala Ala Thr Val Cys Ser Ala Leu Tyr Ile Gly Asp Leu Cys
80 85 90
Gly Gly Val Phe Leu Val Gly Gln Met Phe Ser Phe Gln Pro Arg
95 100 105
Arg His Trp Thr Thr Gln Asp Cys Asn Cys Ser Ile Tyr Ala Gly
110 115 120
His Val Thr Gly His Arg Met Ala Trp Asp Met Met Met Asn Trp
125 130 135
Ser Pro Thr Thr Thr Leu Val Leu Ala Gln Val Met Arg Ile Pro
140 145 150
Ser Thr Leu Val Asp Leu Leu Thr Gly Gly His Trp Gly Ile Leu
155 160 165
Ile Gly Val Ala Tyr Phe Cys Met Gln Ala Asn Trp Ala Lys Val
170 175 180
Ile Leu Val Leu Phe Leu Tyr Ala Gly Val Asp Ala
185 190

(2) INFORMATION FOR SEQ ID NO:95:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 192 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: unknown
(D) TOPOLOGY: unknown

(vi) ORIGINAL SOURCE:
(A) ORGANISM: homosapiens
(C) INDIVIDUAL ISOLATE: DK13

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:95:

Tyr Asn Tyr Arg Asn Ser Ser Gly Val Tyr His Val Thr Asn Asp
5 10 15
Cys Pro Asn Ser Ser Ile Val Tyr Glu Thr Asp Tyr His Ile Leu
20 25 30
His Leu Pro Gly Cys Val Pro Cys Val Arg Glu Gly Asn Lys Ser
35 40 45
Thr Cys Trp Val Ser Leu Thr Pro Thr Val Ala Ala Gln His Leu
50 55 60
Asn Ala Pro Leu Glu Ser Leu Arg Arg His Val Asp Leu Met Val
65 70 75
Gly Gly Ala Thr Leu Cys Ser Ala Leu Tyr Ile Gly Asp Val Cys
80 85 90
Gly Gly Val Phe Leu Val Gly Gln Leu Phe Thr Phe Gln Pro Arg
95 100 105
Arg His Trp Thr Thr Gln Asp Cys Asn Cys Ser Ile Tyr Thr Gly
110 115 120
His Ile Thr Gly His Arg Met Ala Trp Asp Met Met Met Asn Trp
125 130 135
Ser Pro Thr Ala Thr Leu Val Leu Ala Gln Leu Met Arg Ile Pro
140 145 150
Gly Ala Met Val Asp Leu Leu Ala Gly Gly His Trp Gly Ile Leu
155 160 165

Val Gly Ile Ala Tyr Phe Ser Met Gln Ala Asn Trp Ala Lys Val
170 175 180
Ile Leu Val Leu Phe Leu Phe Ala Gly Val Asp Ala
185 190

(2) INFORMATION FOR SEQ ID NO:96:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 192 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: unknown
(D) TOPOLOGY: unknown

(vi) ORIGINAL SOURCE:
(A) ORGANISM: homosapiens
(C) INDIVIDUAL ISOLATE: SA1

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:96:

Val Pro Tyr Arg Asn Ala Ser Gly Val Tyr His Val Thr Asn Asp
5 10 15
Cys Pro Asn Ser Ser Ile Val Tyr Glu Ala Asp Ser Leu Ile Leu
20 25 30
His Ala Pro Gly Cys Val Pro Cys Val Arg Gln Asp Asn Val Ser
35 40 45
Arg Cys Trp Val Gln Ile Thr Pro Thr Leu Ser Ala Pro Thr Phe
50 55 60
Gly Ala Val Thr Ala Pro Leu Arg Arg Ala Val Asp Tyr Leu Ala
65 70 75
Gly Gly Ala Ala Leu Cys Ser Ala Leu Tyr Val Gly Asp Ala Cys
80 85 90
Gly Ala Val Phe Leu Val Gly Gln Met Phe Thr Tyr Arg Pro Arg
95 100 105
Gln His Thr Thr Val Gln Asp Cys Asn Cys Ser Ile Tyr Ser Gly
110 115 120
His Ile Thr Gly His Arg Met Ala Trp Asp Met Met Met Asn Trp
125 130 135
Ser Pro Thr Thr Ala Leu Leu Met Ala Gln Met Leu Arg Ile Pro
140 145 150
Gln Val Val Ile Asp Ile Ile Ala Gly Gly His Trp Gly Val Leu
155 160 165
Phe Ala Ala Ala Tyr Phe Ala Ser Ala Ala Asn Trp Ala Lys Val
170 175 180
Val Leu Val Leu Phe Leu Phe Ala Gly Val Asp Gly
185 190

(2) INFORMATION FOR SEQ ID NO:97:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 192 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: unknown
(D) TOPOLOGY: unknown

(vi) ORIGINAL SOURCE:
(A) ORGANISM: homosapiens
(C) INDIVIDUAL ISOLATE: SA4

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:97:

Val Pro Tyr Arg Asn Ala Ser Gly Val Tyr His Val Thr Asn Asp
5 10 15
Cys Pro Asn Ser Ser Ile Val Tyr Glu Ala Asp Asn Leu Ile Leu
20 25 30
His Ala Pro Gly Cys Val Pro Cys Val Arg Gln Asp Asn Val Ser
35 40 45
Lys Cys Trp Val Gln Ile Thr Pro Thr Leu Ser Ala Pro Asn Leu
50 55 60
Gly Ala Val Thr Ala Pro Leu Arg Arg Ala Val Asp Tyr Leu Ala
65 70 75
Gly Gly Ala Ala Leu Cys Ser Ala Leu Tyr Val Gly Asp Ala Cys
80 85 90
Gly Ala Val Phe Leu Val Gly Gln Met Phe Thr Tyr Arg Pro Arg
95 100 105
Gln His Thr Thr Val Gln Asp Cys Asn Cys Ser Ile Tyr Ser Gly
110 115 120
His Ile Thr Gly His Arg Met Ala Trp Asp Met Met Met Asn Trp
125 130 135
Ser Pro Thr Thr Ala Leu Leu Met Ala Gln Leu Leu Arg Ile Pro
140 145 150
Gln Val Val Ile Asp Ile Ile Ala Gly Gly His Trp Gly Val Leu
155 160 165
Phe Ala Ala Ala Tyr Phe Ala Ser Ala Ala Asn Trp Ala Lys Val
170 175 180
Ile Leu Val Leu Phe Leu Phe Ala Gly Val Asp Ala
185 190

(2) INFORMATION FOR SEQ ID NO:98:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 192 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: unknown
(D) TOPOLOGY: unknown

(vi) ORIGINAL SOURCE:
(A) ORGANISM: homosapiens
(C) INDIVIDUAL ISOLATE: SA5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:98:

Val Pro Tyr Arg Asn Ala Ser Gly Val Tyr His Val Thr Asn Asp
5 10 15
Cys Pro Asn Ser Ser Ile Val Tyr Glu Ala Asp Asn Leu Ile Leu
20 25 30
His Ala Pro Gly Cys Val Pro Cys Val Lys Glu Gly Asn Val Ser
35 40 45

Arg Cys Trp Val Gln Ile Thr Pro Thr Leu Ser Ala Pro Asn Leu
50 55 60
Gly Ala Val Thr Ala Pro Leu Arg Arg Val Val Asp Tyr Leu Ala
65 70 75
Gly Gly Ala Ala Leu Cys Ser Ala Leu Tyr Val Gly Asp Ala Cys
80 85 90
Gly Ala Val Phe Leu Val Gly Gln Met Phe Thr Tyr Arg Pro Arg
95 100 105
Gln His Thr Thr Val Gln Asp Cys Asn Cys Ser Ile Tyr Ser Gly
110 115 120
His Ile Thr Gly His Arg Met Ala Trp Asp Met Met Met Asn Trp
125 130 135
Ser Pro Thr Thr Ala Leu Val Met Ala Gln Val Leu Arg Ile Pro
140 145 150
Gln Val Val Ile Asp Ile Ile Ala Gly Gly His Trp Gly Val Leu
155 160 165
Phe Ala Val Ala Tyr Phe Ala Ser Ala Ala Asn Trp Ala Lys Val
170 175 180
Val Leu Val Leu Phe Leu Phe Ala Gly Val Asp Gly
185 190

(2) INFORMATION FOR SEQ ID NO:99:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 192 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: unknown
(D) TOPOLOGY: unknown

(vi) ORIGINAL SOURCE:
(A) ORGANISM: homosapiens
(C) INDIVIDUAL ISOLATE: SA6

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:99:

Val Pro Tyr Arg Asn Ala Ser Gly Val Tyr His Val Thr Asn Asp
5 10 15
Cys Pro Asn Ser Ser Ile Val Tyr Glu Ala Asp Asp Leu Ile Leu
20 25 30
His Ala Pro Gly Cys Val Pro Cys Val Arg Lys Asp Asn Val Ser
35 40 45
Arg Cys Trp Val His Ile Thr Pro Thr Leu Ser Ala Pro Ser Leu
50 55 60
Gly Ala Val Thr Ala Pro Leu Arg Arg Ala Val Asp Tyr Leu Ala
65 70 75
Gly Gly Ala Ala Leu Cys Ser Ala Leu Tyr Val Gly Asp Val Cys
80 85 90
Gly Ala Leu Phe Leu Val Gly Gln Met Phe Thr Tyr Arg Pro Arg
95 100 105
Gln His Ala Thr Val Gln Asp Cys Asn Cys Ser Ile Tyr Ser Gly
110 115 120
His Ile Thr Gly His Arg Met Ala Trp Asp Met Met Met Asn Trp
125 130 135

Ser Pro Ala Thr Ala Leu Val Met Ala Gln Met Leu Arg Ile Pro
140 145 150
Gln Val Val Ile Asp Ile Ile Ala Gly Gly His Trp Gly Val Leu
155 160 165
Phe Ala Ala Ala Tyr Phe Ala Ser Ala Ala Asn Trp Ala Lys Val
170 175 180
Val Leu Val Leu Phe Leu Phe Ala Gly Val Asp Ala
185 190

(2) INFORMATION FOR SEQ ID NO:100:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 192 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: unknown
(D) TOPOLOGY: unknown

(vi) ORIGINAL SOURCE:
(A) ORGANISM: homosapiens
(C) INDIVIDUAL ISOLATE: SA7

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:100:

Val Pro Tyr Arg Asn Ala Ser Gly Val Tyr His Val Thr Asn Asp
5 10 15
Cys Pro Asn Ser Ser Ile Val Tyr Glu Ala Asp Asn Leu Ile Leu
20 25 30
His Ala Pro Gly Cys Val Pro Cys Val Arg Gln Asn Asn Val Ser
35 40 45
Arg Cys Trp Val Gln Ile Thr Pro Thr Leu Ser Ala Pro Asn Leu
50 55 60
Gly Ala Val Thr Ala Pro Leu Arg Arg Ala Val Asp Tyr Leu Ala
65 70 75
Gly Gly Ala Ala Leu Cys Ser Ala Leu Tyr Val Gly Asp Ala Cys
80 85 90
Gly Ala Val Phe Leu Val Gly Gln Met Phe Ser Tyr Arg Pro Arg
95 100 105
Gln His Thr Thr Val Gln Asp Cys Asn Cys Ser Ile Tyr Ser Gly
110 115 120
His Ile Thr Gly His Arg Met Ala Trp Asp Met Met Met Asn Trp
125 130 135
Ser Pro Thr Thr Ala Leu Val Met Ala Gln Leu Leu Arg Ile Pro
140 145 150
Gln Val Val Ile Asp Ile Ile Ala Gly Gly His Trp Gly Val Leu
155 160 165
Phe Ala Ala Ala Tyr Phe Ala Ser Ala Ala Asn Trp Ala Lys Val
170 175 180
Val Leu Val Leu Phe Leu Phe Ala Gly Val Asp Ala
185 190

(2) INFORMATION FOR SEQ ID NO:101:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 192 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: unknown
(D) TOPOLOGY: unknown

(vi) ORIGINAL SOURCE:
(A) ORGANISM: homosapiens
(C) INDIVIDUAL ISOLATE: SA13

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:101:

Val Pro Tyr Arg Asn Ala Ser Gly Val Tyr His Val Thr Asn Asp
5 10 15
Cys Pro Asn Ser Ser Ile Val Tyr Glu Ala Asp Asp Leu Ile Leu
20 25 30
His Ala Pro Gly Cys Val Pro Cys Val Arg Gln Gly Asn Val Ser
35 40 45
Arg Cys Trp Val Gln Ile Thr Pro Thr Leu Ser Ala Pro Ser Leu
50 55 60
Gly Ala Val Thr Ala Pro Leu Arg Arg Ala Val Asp Tyr Leu Ala
65 70 75
Gly Gly Ala Ala Leu Cys Ser Ala Leu Tyr Val Gly Asp Ala Cys
80 85 90
Gly Ala Val Phe Leu Val Gly Gln Met Phe Thr Tyr Ser Pro Arg
95 100 105
Arg His Asn Val Val Gln Asp Cys Asn Cys Ser Ile Tyr Ser Gly
110 115 120
His Ile Thr Gly His Arg Met Ala Trp Asp Met Met Met Asn Trp
125 130 135
Ser Pro Thr Thr Ala Leu Val Met Ala Gln Leu Leu Arg Ile Pro
140 145 150
Gln Val Val Ile Asp Ile Ile Ala Gly Ala His Trp Gly Val Leu
155 160 165
Phe Ala Ala Ala Tyr Tyr Ala Ser Ala Ala Asn Trp Ala Lys Val
170 175 180
Val Leu Val Leu Phe Leu Phe Ala Gly Val Asp Ala
185 190

(2) INFORMATION FOR SEQ ID NO:102:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 192 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: unknown
(D) TOPOLOGY: unknown

(vi) ORIGINAL SOURCE:
(A) ORGANISM: homosapiens
(C) INDIVIDUAL ISOLATE: HK2

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:102:

Leu Thr Tyr Gln Asn Ser Ser Gln Leu Tyr His Leu Thr Asn Asp
1 10 15
Cys Pro Asn Ser Ser Ile Val Leu Glu Ala Asp Ala Met Ile Leu
20 25 30
His Leu Pro Gln Cys Leu Pro Cys Val Arg Val Asp Asp Arg Ser
35 40 45
Thr Cys Trp His Ala Val Thr Pro Thr Leu Ala Ile Pro Asn Ala
50 55 60
Ser Thr Pro Ala Thr Gln Phe Arg Arg His Val Asp Leu Leu Ala
65 70 75
Gln Ala Ala Val Val Cys Ser Ser Leu Tyr Ile Gln Asp Leu Cys
80 85 90
Gln Ser Leu Phe Leu Ala Gln Gln Leu Phe Thr Phe Gln Pro Arg
95 100 105
Arg His Trp Thr Val Gln Asp Cys Asn Cys Ser Ile Tyr Thr Gln
110 115 120
His Val Thr Gln His Arg Met Ala Trp Asp Met Met Met Asn Trp
125 130 135
Ser Pro Thr Thr Thr Leu Val Leu Ser Ser Ile Leu Arg Val Pro
140 145 150
Glu Ile Cys Ala Ser Val Ile Phe Gln Gln His Trp Gln Ile Leu
155 160 165
Leu Ala Val Ala Tyr Phe Gln Met Ala Gln Asn Trp Leu Lys Val
170 175 180
Leu Ala Val Leu Phe Leu Phe Ala Gln Val Glu Ala
185 190

(2) INFORMATION FOR SEQ ID NO:103:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 40 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:103:

GCGTCCGGGT TCTGGAAGAC GGCGTGAACT ATGCAACAGG 40

(2) INFORMATION FOR SEQ ID NO:104:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 40 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:104:

AGGCTTTCAT TGCAGTTCAA GGCCGTGCTA TTGATGTGCC 40

(2) INFORMATION FOR SEQ ID NO:105:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 40 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:105:

AAGACGGCGT GAACTATGCA ACAGGGAACC TTCCTGGTTG 40

(2) INFORMATION FOR SEQ ID NO:106:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 40 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:106:

AGTTCAAGGC CGTGCTATTG ATGTGCCAAC TGCCGTTGGT 40

(2) INFORMATION FOR SEQ ID NO:107:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 40 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:107:

AAGACGGCGT GAATTCTGCA ACAGGGAACC TTCCTGGTTG 40

(2) INFORMATION FOR SEQ ID NO:108:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 40 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:108:

AGTTCAAGGC CGTGGAATTC ATGTGCCAAC TGCCGTTGGT 40

(2) INFORMATION FOR SEQ ID NO:109:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 42 base pairs

(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:109:

ARCTYCGACG TYACATCGAY CTGCTYGTYG GRAGYGCCAC CC 42

(2) INFORMATION FOR SEQ ID NO:110:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 31 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:110:

RCARGCCRTC TTGGAYATGA TCGCTGGWGC Y 31

(2) INFORMATION FOR SEQ ID NO:111:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 42 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:111:

CRATACGACR YCAYGTCGAY TTGCTCGTTG GGGCGGCTRY YT 42

(2) INFORMATION FOR SEQ ID NO:112:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 31 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:112:

RCAAGCTRTC RTGGAYRTGG TRRCRGGRGC C 31

(2) INFORMATION FOR SEQ ID NO:113:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 40 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:113:

TTGCGGACKC ACATYGACAT GGTYGTGATG TCCGCCACGC 40

(2) INFORMATION FOR SEQ ID NO:114:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 43 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:114:

GATGCGCGTT CCCGAGGTCA TCWTAGACAT CRTYRGCGGR GCD 43

(2) INFORMATION FOR SEQ ID NO:115:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 54 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:115:

AATGGCACCY TGCRCTGCTG GATACAAGTR ACACCTAATG TGGCTGTGAA 50
ACAC 54

(2) INFORMATION FOR SEQ ID NO:116:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 31 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:116:

ARCTAGYC CTYSARGTYG TCTTCGGYGG Y 31

(2) INFORMATION FOR SEQ ID NO:117:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 54 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:117:

GCCAACGTCT CTCGATGTTG GGTGCCGGTT GCCCCCAATC TCGCCATAAG 50
TCAA 54

(2) INFORMATION FOR SEQ ID NO:118:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 46 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:118:

AAGGGCCTGC GAGCACACAT CGATATCATC GTGATGTCTG CTACGG 46

(2) INFORMATION FOR SEQ ID NO:119:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 45 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:119:

TTGGTGCGCA TCCCGGAAGT CATCTTGGAT ATTGTTACAG GAGGT 45

(2) INFORMATION FOR SEQ ID NO:120:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 40 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:120:

AGTCAGGTAY GTCGGAGCAA CCACCGCYTC GATACGCAGT 40

(2) INFORMATION FOR SEQ ID NO:121:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 46 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:121:

AGCCTTCACG TTCAGACCKC GTCGCCATCA AACRGTCCAG ACCTGT 46

(2) INFORMATION FOR SEQ ID NO:122:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 75 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:122:

TCCCCCGCYG TGGGTATGGT GGTRGCGCAC RTYCTGCGDY TGCCCCAGAC 50
CKTGTTYGAC ATAMTRGCYG GGGCC 75

(2) INFORMATION FOR SEQ ID NO:123:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 39 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:123:

ACGCCGGTGA CGCCTACAGT GGCTGTCGCA CACCCGGGC 39

(2) INFORMATION FOR SEQ ID NO:124:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 42 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:124:

ATGAGGGTCC CCACAGCCTT TCTCGACATG GTTGCCGGAG GC 42

(2) INFORMATION FOR SEQ ID NO:125:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 40 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:125:

CGCGCCCTAT CCCAACGCAC CGTTAGAGTC CATGCGCAGG 40

(2) INFORMATION FOR SEQ ID NO:126:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 49 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:126:

TCAGATCTTA CGGATCCCCT CTATCCTAGG TGACTTGCTC ACCGGGGGT 49

(2) INFORMATION FOR SEQ ID NO:127:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 54 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:127:

CAGTCACGCT GCTGGGTGGC CCTTACTCCC ACCGTGGCGG YGYCTTATAT 50
CGGT 54

(2) INFORMATION FOR SEQ ID NO:128:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 31 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:128:

TAGCACTCTG GTRGAYCTAC TCRCTGGAGG G 31

(2) INFORMATION FOR SEQ ID NO:129:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 54 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:129:

AAGTCTACAT GCTGGGTGTC TCTCACCCCC ACCGTGGCTG CGCAACATCT 50
GAAT 54

(2) INFORMATION FOR SEQ ID NO:130:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 31 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:130:

AGGCGCCATG GTCGACCTGC TTGCAGGCGG C 31

(2) INFORMATION FOR SEQ ID NO:131:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 43 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:131:

TCAGCCCCGA VYYTCGGAGC GGTCACGGCT CCTCTTCGGA GGG 43

(2) INFORMATION FOR SEQ ID NO:132:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 44 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:132:

TGYTACGGAT YCCCCARGTG GTCATHGACA TCATWGCCGG GGSC 44

(2) INFORMATION FOR SEQ ID NO:133:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 40 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:133:

CATACCAAAT GCTTCCACGC CCGCAACGGG ATTCCGCAGG 40

(2) INFORMATION FOR SEQ ID NO:134:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 37 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:134:

TCTTCTTGCG GGCGCCGCAG TGGTTTGCTC ATCCCTG 37

(2) INFORMATION FOR SEQ ID NO:135:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 52 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:135:

ATCTAGCATC TTGAGGGTAC CTGAGATTTG TGCGAGTGTG ATATTTGGTG 50
GC 52

(2) INFORMATION FOR SEQ ID NO:136:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 33 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: unknown
(D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:136:

Trp Ile Gln Val Thr Pro Asn Val Ala Val Lys His Arg Gly Ala
5 10 15
Leu Thr His Asn Leu Arg Xaa His Xaa Asp Xaa Ile Val Met Ala
20 25 30
Ala Thr Val

(2) INFORMATION FOR SEQ ID NO:137:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 33 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: unknown
(D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:137:

Trp Val Pro Val Ala Pro Asn Leu Ala Ile Ser Gln Pro Gly Ala
5 10 15

Leu Thr Lys Gly Leu Arg Ala His Ile Asp Ile Ile Val Met Ser
20 25 30
Ala Thr Val

(2) INFORMATION FOR SEQ ID NO:138:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 33 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: unknown
(D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:138:

Trp Ile Pro Val Xaa Pro Asn Val Ala Val Xaa Xaa Pro Gly Ala
5 10 15
Leu Thr Gln Gly Leu Arg Thr His Ile Asp Met Val Val Met Ser
20 25 30
Ala Thr Leu

(2) INFORMATION FOR SEQ ID NO:139:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 33 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: unknown
(D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:139:

Trp Thr Xaa Val Thr Pro Thr Val Ala Val Arg Tyr Val Gly Ala
5 10 15
Thr Thr Ala Ser Ile Arg Ser His Val Asp Leu Leu Val Gly Ala
20 25 30
Ala Thr Xaa

(2) INFORMATION FOR SEQ ID NO:140:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 33 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: unknown
(D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:140:

Trp Val Ala Leu Xaa Pro Thr Leu Ala Ala Arg Asn Xaa Xaa Xaa
5 10 15
Xaa Thr Xaa Xaa Ile Arg Xaa His Val Asp Leu Leu Val Gly Ala
20 25 30
Ala Xaa Phe

(2) INFORMATION FOR SEQ ID NO:141:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 33 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: unknown
(D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:141:

Trp Val Xaa Xaa Xaa Pro Thr Val Ala Thr Arg Asp Gly Lys Leu
5 10 15
Pro Xaa Xaa Gln Leu Arg Arg Xaa Ile Asp Leu Leu Val Gly Ser
20 25 30
Ala Thr Leu

(2) INFORMATION FOR SEQ ID NO:142:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 33 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: unknown
(D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:142:

Trp Thr Pro Val Thr Pro Thr Val Ala Val Ala His Pro Gly Ala
5 10 15
Pro Leu Glu Ser Phe Arg Arg His Val Asp Leu Met Val Gly Ala
20 25 30
Ala Thr Leu

(2) INFORMATION FOR SEQ ID NO:143:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 33 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: unknown
(D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:143:

Trp Val Ala Leu Thr Pro Thr Val Ala Xaa Xaa Tyr Ile Gly Ala
5 10 15
Pro Leu Xaa Ser Xaa Arg Arg His Val Asp Leu Met Val Gly Ala
20 25 30
Ala Thr Val

(2) INFORMATION FOR SEQ ID NO:144:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 33 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: unknown
(D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:144:

Trp Val Ser Leu Thr Pro Thr Val Ala Ala Gln His Leu Asn Ala
5 10 15
Pro Leu Glu Ser Leu Arg Arg His Val Asp Leu Met Val Gly Gly
20 25 30
Ala Thr Leu

(2) INFORMATION FOR SEQ ID NO:145:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 33 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: unknown
(D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:145:

Trp Val Pro Leu Thr Pro Thr Val Ala Ala Pro Tyr Pro Asn Ala
5 10 15
Pro Leu Glu Ser Met Arg Arg His Val Asp Leu Met Val Gly Ala
20 25 30
Ala Thr Met

(2) INFORMATION FOR SEQ ID NO:146:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 33 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: unknown
(D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:146:

Trp Val Xaa Ile Thr Pro Thr Leu Ser Ala Pro Xaa Xaa Gly Ala
5 10 15
Val Thr Ala Pro Leu Arg Arg Xaa Val Asp Tyr Leu Ala Gly Gly
20 25 30
Ala Ala Leu

(2) INFORMATION FOR SEQ ID NO:147:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 33 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: unknown
(D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:147:

Trp His Ala Val Thr Pro Thr Leu Ala Ile Pro Asn Ala Ser Thr
5 10 15
Pro Ala Thr Gly Phe Arg Arg His Val Asp Leu Leu Ala Gly Ala
20 25 30
Ala Val Val

(2) INFORMATION FOR SEQ ID NO:148:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 23 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: unknown
(D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:148:

Thr Leu Thr Met Ile Leu Ala Tyr Ala Ala Arg Val Pro Glu Leu
5 10 15
Xaa Leu Xaa Val Val Phe Gly Gly
20

(2) INFORMATION FOR SEQ ID NO:149:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 23 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: unknown
(D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:149:

Thr Thr Thr Met Leu Leu Ala Tyr Leu Val Arg Ile Pro Glu Val
5 10 15
Ile Leu Asp Ile Val Thr Gly Gly
20

(2) INFORMATION FOR SEQ ID NO:150:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 23 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: unknown
(D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:150:

Thr Xaa Thr Xaa Ile Leu Ala Tyr Xaa Met Arg Val Pro Glu Val
5 10 15
Ile Xaa Asp Ile Xaa Xaa Gly Ala
20

(2) INFORMATION FOR SEQ ID NO:151:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 23 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: unknown
(D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:151:

Ala Val Gly Met Val Val Ala His Xaa Leu Arg Leu Pro Gln Thr
5 10 15
Xaa Phe Asp Ile Xaa Ala Gly Ala
20

(2) INFORMATION FOR SEQ ID NO:152:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 23 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: unknown
(D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:152:

Thr Xaa Ala Leu Val Xaa Ser Gln Leu Leu Arg Xaa Pro Gln Ala
5 10 15
Xaa Xaa Asp Xaa Val Xaa Gly Ala
20

(2) INFORMATION FOR SEQ ID NO:153:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 23 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: unknown
(D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:153:

Thr Xaa Ala Leu Val Xaa Ala Gln Leu Leu Arg Xaa Pro Gln Ala
5 10 15
Xaa Leu Asp Met Ile Ala Gly Ala
20

(2) INFORMATION FOR SEQ ID NO:154:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 23 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: unknown

(D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:154:

Thr Thr Thr Leu Leu Leu Ala Gln Ile Met Arg Val Pro Thr Ala
5 10 15
Phe Leu Asp Met Val Ala Gly Gly
20

(2) INFORMATION FOR SEQ ID NO:155:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 23 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: unknown
(D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:155:

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5 10 15
Leu Val Asp Leu Leu Xaa Gly Gly
20

(2) INFORMATION FOR SEQ ID NO:156:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 23 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: unknown
(D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:156:

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5 10 15
Met Val Asp Leu Leu Ala Gly Gly
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(2) INFORMATION FOR SEQ ID NO:157:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 23 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: unknown
(D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:157:

Thr Ser Ala Leu Ile Met Ala Gln Ile Leu Arg Ile Pro Ser Ile
5 10 15

Leu Gly Asp Leu Leu Thr Gly Gly
20

(2) INFORMATION FOR SEQ ID NO:158:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 23 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: unknown
(D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:158:

Xaa Thr Ala Leu Xaa Met Ala Gln Xaa Leu Arg Ile Pro Gln Val
5 10 15
Val Ile Asp Ile Ile Ala Gly Xaa
20

(2) INFORMATION FOR SEQ ID NO:159:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 23 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: unknown
(D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:159:

Thr Thr Thr Leu Val Leu Ser Ser Ile Leu Arg Val Pro Glu Ile
5 10 15
Cys Ala Ser Val Ile Phe Gly Gly
20

CLAIMS

1. A cDNA of the envelope 1 gene of the hepatitis C virus wherein the cDNA has a sequence selected from the group consisting of SEQ ID NO:1 through SEQ ID NO:51.

2. A recombinant hepatitis C virus envelope 1 protein encoded by a gene whose sequence includes a sequence selected from the group consisting of SEQ ID NO:1 through SEQ ID NO:51.

3. A recombinant protein having an amino acid sequence selected from the group consisting of SEQ ID NO:52 through SEQ ID NO:102.

4. A method for the recombinant DNA-directed synthesis of at least one complete envelope 1 protein of hepatitis C virus said method comprising:

culturing a transformed or transfected host organism containing a DNA sequence capable of directing the host organism to produce an envelope 1 protein under conditions such that the protein is produced, said protein exhibiting substantial homology to a protein comprising the amino acid sequence selected from the group consisting of SEQ ID NO:52 through SEQ ID NO:102.

5. The method of claim 4, wherein the host organism is transfected with a recombinant eukaryotic expression vector.

6. The method of claim 4, wherein the eukaryotic vector is a baculovirus vector.

7. The method of claim 4, wherein the host

organism is a eukaryotic cell.

8. The method of claim 7, wherein the eukaryotic cell is an insect cell.

9. A recombinant expression vector comprising a cDNA sequence selected from the group consisting of SEQ ID NO:1 through SEQ ID NO:51.

10. A host organism transformed or transfected with a recombinant expression vector according to claim 9.

11. A method of detecting antibodies to HCV in a biological sample suspected of containing said antibodies comprising:

(a) contacting the sample with at least one recombinant protein of claim 3 to form an immune complex with the antibodies; and

(b) detecting the presence of the immune complex.

12. The method of claim 11 wherein the biological sample is selected from the group consisting of serum, saliva or lymphocytes or other mononuclear cells.

13. The method of claim 11, wherein the recombinant envelope 1 protein is bound to a solid support.

14. The method of claim 11, wherein the immune complex is detected using a labeled antibody.

15. A hepatitis C virus hit comprising: at least one recombinant protein comprising an amino acid sequence selected from the group consisting of: SEQ ID NO:52 through SEQ ID NO:102.

16. A pharmaceutical composition comprising at least one recombinant protein of claim 3 and a suitable excipient, diluent or carrier.

17. A method of preventing hepatitis C infection, comprising administering the pharmaceutical composition of claim 16 to a mammal in an effective amount to stimulate the production of protective antibody.

18. A vaccine for immunizing a mammal against hepatitis C infection, comprising at least one recombinant protein according to claim 3 in a pharmacologically acceptable carrier.

19. A method for detecting the presence of the hepatitis C virus via a reverse transcription-polymerase chain reaction process, wherein the primers are selected from the sequences shown in SEQ ID NO:103 through in SEQ ID NO:108.

20. Substantially isolated and purified primers, wherein said primers have nucleic acid sequences selected from the group consisting of SEQ ID NO:103 through SEQ ID NO:108.

21. A diagnostic kit for use in detecting the presence of hepatitis C virus, said kit comprising: primers having nucleic acid sequences selected from the group consisting of SEQ ID NO:103 through SEQ ID NO:108.

22. A method for determining the genotype of a hepatitis C virus, said method comprising:

(a) amplifying RNA via reverse transcription-polymerase chain reaction to produce amplification products;

(b) contacting said products with at least

one genotype-specific oligonucleotide; and

(c) detecting complexes of said products which bind to said oligonucleotide(s).

23. The method of claim 22, wherein said amplification of step (a) uses primer having a sequence according to SEQ ID NO:103 through SEQ ID NO:108.

24. The method of claim 23, wherein said oligonucleotide of the step (b) is a nucleic acid sequence selected from the group consisting of SEQ ID NO:109 through SEQ ID NO:135.

25. Substantially isolated and purified oligonucleotides, wherein said oligonucleotides have nucleic acid sequences selected from the group consisting of SEQ ID NO:109 through SEQ ID NO:135.

26. A diagnostic kit for determining the genotype of a hepatitis C virus, said kit comprising primers selected from the group consisting of SEQ ID NO:103 through SEQ ID NO:108 and hybridization probes selected from the group consisting of SEQ ID NO:109 through SEQ ID NO:135.

27. A substantially purified and isolated peptide having an amino acid sequence selected from the group consisting of SEQ ID NO:136 through SEQ ID NO:159.

28. A method of detecting antibodies specific for a single genotype of HCV, said method comprising:

(a) contacting a biological sample with at least one peptide of claim 27 to form an immune complex with the antibodies, and

(b) detecting the presence of the immune complex.

29. The method of claim 28, wherein the biological sample is selected from the group consisting of serum, saliva or lymphocytes or other mononuclear cells.

30. The method of claim 28, wherein said peptide is bound to a solid support.

31. The method of claim 28, wherein the immune complex is detected using a labelled antibody.

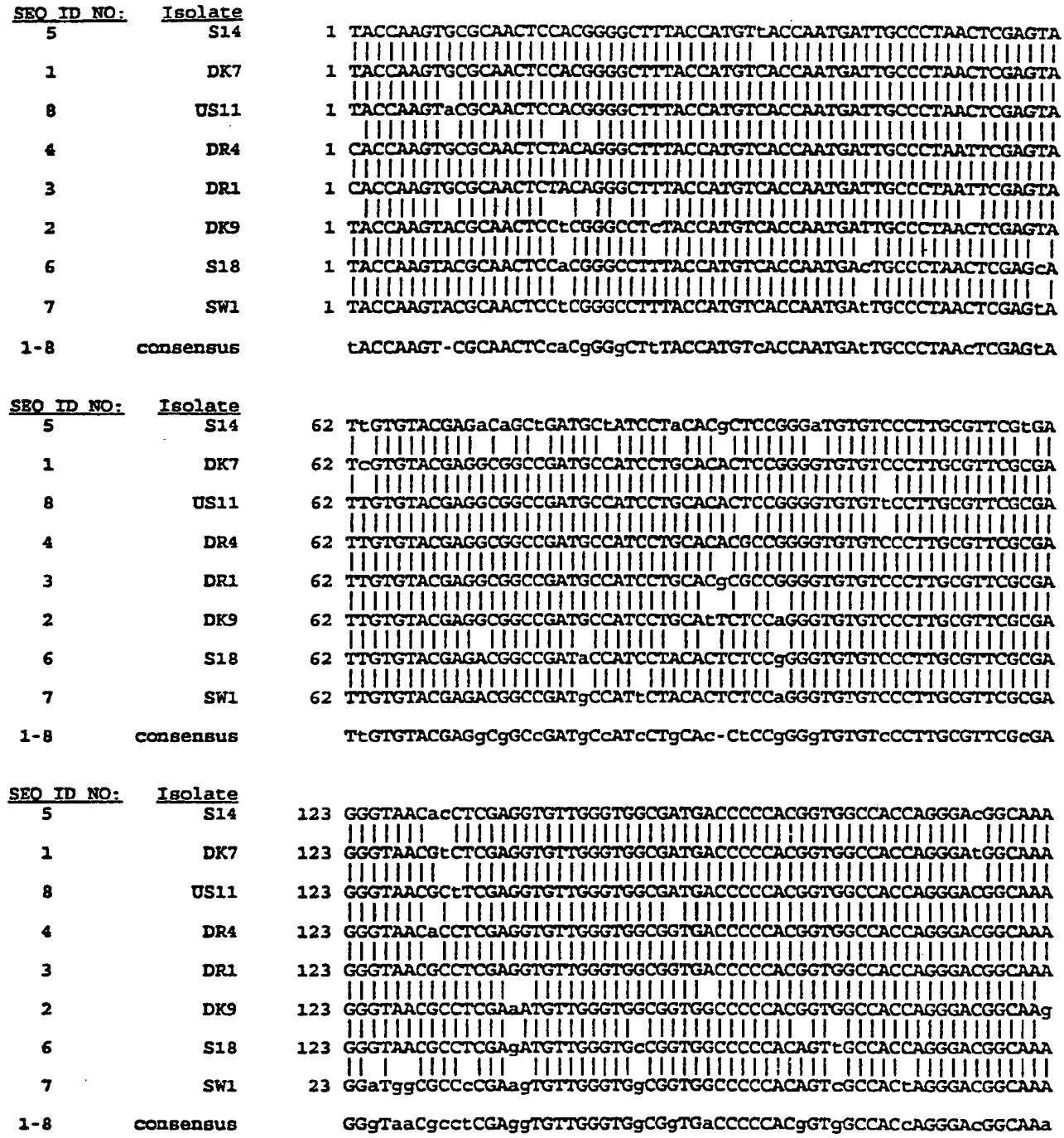
32. A kit for use in detecting hepatitis C virus antibodies, said kit comprising: at least one peptide selected from the group consisting of SEQ ID NO:136 through SEQ ID NO:159.

33. A pharmaceutical composition comprising at least one peptide of claim 27 and a suitable excipient, diluent or carrier.

34. A method of preventing hepatitis C infection, comprising administering the pharmaceutical composition of claim 33 to a mammal in an effective amount to stimulate production of a protective antibody.

35. A vaccine for immunizing a mammal against hepatitis C infection, comprising at least one peptide according to claim 27 in a pharmaceutically acceptable carrier.

FIGURE 1A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1 DK7 1 TACCAAGTGCGCAACTCCACGGGGCTTTACCATGTCACCAATGATTGCCCTAACTCGAGTA
8 US11 1 TACCAAGTaCGCAACTCCACGGGGCTTTACCATGTCACCAATGATTGCCCTAACTCGAGTA
4 DR4 1 CACCAAGTGCGCAACTCTACAGGGCTTTACCATGTCACCAATGATTGCCCTAATTCGAGTA
3 DR1 1 CACCAAGTGCGCAACTCTACAGGGCTTTACCATGTCACCAATGATTGCCCTAATTCGAGTA
2 DK9 1 TACCAAGTACGCAACTCCtCGGGCCTcTACCATGTCACCAATGATTGCCCTAACTCGAGTA
6 S18 1 TACCAAGTACGCAACTCCaCGGGCCTTTACCATGTCACCAATGAcTGCCCTAACTCGAGcA
7 SW1 1 TACCAAGTACGCAACTCCtCGGGCCTTTACCATGTCACCAATGAtTGCCCTAACTCGAGtA
1-8 consensus tACCAAGT-CGCAACTCcaCgGGgCTtTACCATGTcACCAATGAtTGCCCTAAcTCGAGtA
SEQ ID NO: Isolate
5 S14 62 TtGTGTACGAGaCaGCtGATGCtATCCTaCACgCTCCGGGaTGTGTCCCTTGCGTTCGtGA
1 DK7 62 TcGTGTACGAGGCGGCCGATGCCATCCTGCACACTCCGGGGTGTGTCCCTTGCGTTCGCGA
8 US11 62 TTGTGTACGAGGCGGCCGATGCCATCCTGCACACTCCGGGGTGTGTtCCTTGCGTTCGCGA
4 DR4 62 TTGTGTACGAGGCGGCCGATGCCATCCTGCACACGCCGGGGTGTGTCCCTTGCGTTCGCGA
3 DR1 62 TTGTGTACGAGGCGGCCGATGCCATCCTGCACgCGCCGGGGTGTGTCCCTTGCGTTCGCGA
2 DK9 62 TTGTGTACGAGGCGGCCGATGCCATCCTGCAtTCTCCaGGGTGTGTCCCTTGCGTTCGCGA
6 S18 62 TTGTGTACGAGACGGCCGATaCCATCCTACACTCTCCgGGGTGTGTCCCTTGCGTTCGCGA
7 SW1 62 TTGTGTACGAGACGGCCGATgCCATtCTACACTCTCCaGGGTGTGTCCCTTGCGTTCGCGA
1-8 consensus TtGTGTACGAGgCgGCcGATgCcATcCTgCAc-CtCCgGGgTGTGTcCCTTGCGTTCGcGA
SEQ ID NO: Isolate
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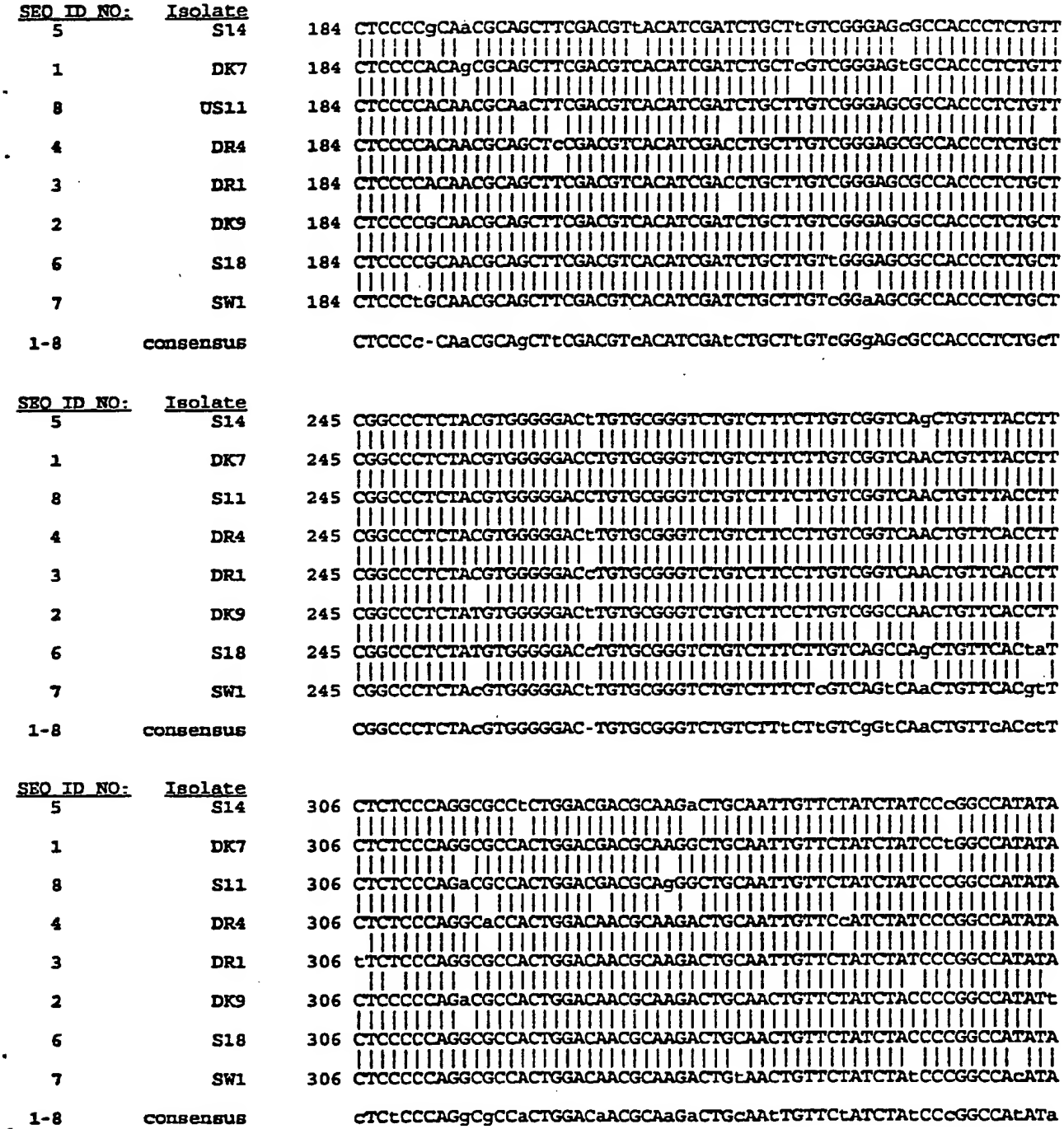
1 DK7 123 GGGTAACGtCTCGAGGTGTTGGGTGGCGATGACCCCCACGGTGGCCACCAGGGAtGGCAAA
8 US11 123 GGGTAACGCtTCGAGGTGTTGGGTGGCGATGACCCCCACGGTGGCCACCAGGGACGGCAAA
4 DR4 123 GGGTAACaCCTCGAGGTGTTGGGTGGCGGTGACCCCCACGGTGGCCACCAGGGACGGCAAA
3 DR1 123 GGGTAACGCCTCGAGGTGTTGGGTGGCGGTGACCCCCACGGTGGCCACCAGGGACGGCAAA
2 DK9 123 GGGTAACGCCTCGAaATGTTGGGTGGCGGTGGCCCCCACGGTGGCCACCAGGGACGGCAAg
6 S18 123 GGGTAACGCCTCGAgATGTTGGGTGcCGGTGGCCCCCACAGTtGCCACCAGGGACGGCAAA
7 SW1 23 GGaTggCGCCcCGAagTGTTGGGTGgCGGTGGCCCCCACAGTcGCCACtAGGGACGGCAAA
1-8 consensus GGgTaaCgcctCGAggTGTTGGGTGgCGgTGaCCCCCACgGTgGCCACcAGGGAcGGCAAa

FIGURE 1A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1 DK7 184 CTCCCCACAgCGCAGCTTCGACGTCACATCGATCTGCTcGTCGGGAGtGCCACCCTCTGTT
8 US11 184 CTCCCCACAACGCAaCTTCGACGTCACATCGATCTGCTTGTCGGGAGCGCCACCCTCTGTT
4 DR4 184 CTCCCCACAACGCAGCTcCGACGTCACATCGACCTGCTTGTCGGGAGCGCCACCCTCTGCT
3 DR1 184 CTCCCCACAACGCAGCTTCGACGTCACATCGACCTGCTTGTCGGGAGCGCCACCCTCTGCT
2 DK9 184 CTCCCCGCAACGCAGCTTCGACGTCACATCGATCTGCTTGTCGGGAGCGCCACCCTCTGCT
6 S18 184 CTCCCCGCAACGCAGCTTCGACGTCACATCGATCTGCTTGTtGGGAGCGCCACCCTCTGCT
7 SW1 184 CTCCCtGCAACGCAGCTTCGACGTCACATCGATCTGCTTGTcGGaAGCGCCACCCTCTGCT
1-8 consensus CTCCCc-CAaCGCAgCTtCGACGTcACATCGAtCTGCTtGTcGGgAGcGCCACCCTCTGcT
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1 DK7 245 CGGCCCTCTACGTGGGGGACCTGTGCGGGTCTGTCTTTCTTGTCGGTCAACTGTTTACCTT
8 S11 245 CGGCCCTCTACGTGGGGGACCTGTGCGGGTCTGTCTTTCTTGTCGGTCAACTGTTTACCTT
4 DR4 245 CGGCCCTCTACGTGGGGGACtTGTGCGGGTCTGTCTTCCTTGTCGGTCAACTGTTCACCTT
3 DR1 245 CGGCCCTCTACGTGGGGGACcTGTGCGGGTCTGTCTTCCTTGTCGGTCAACTGTTCACCTT
2 DK9 245 CGGCCCTCTATGTGGGGGACtTGTGCGGGTCTGTCTTCCTTGTCGGCCAACTGTTCACCTT
6 S18 245 CGGCCCTCTATGTGGGGGACcTGTGCGGGTCTGTCTTTCTTGTCAGCCAgCTGTTCACtaT
7 SW1 245 CGGCCCTCTAcGTGGGGGACtTGTGCGGGTCTGTCTTTCTcGTCAGtCAaCTGTTCACgtT
1-8 consensus CGGCCCTCTAcGTGGGGGAC-TGTGCGGGTCTGTCTTtCTtGTCgGtCAaCTGTTcACctT
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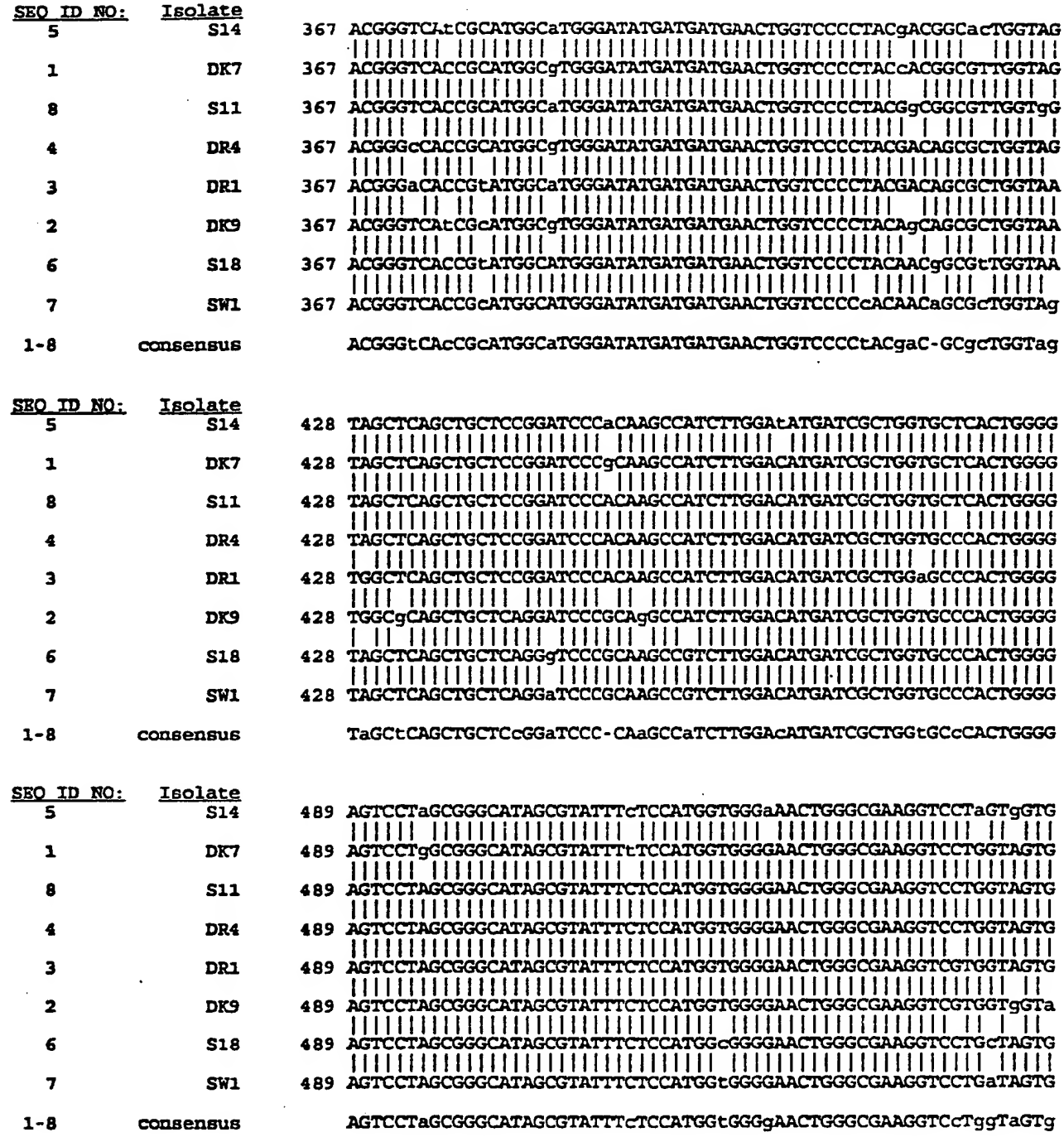
1 DK7 306 CTCTCCCAGGCGCCACTGGACGACGCAAGGCTGCAATTGTTCTATCTATCCtGGCCATATA
8 S11 306 CTCTCCCAGaCGCCACTGGACGACGCAgGGCTGCAATTGTTCTATCTATCCCGGCCATATA
4 DR4 306 CTCTCCCAGGCaCCACTGGACAACGCAAGACTGCAATTGTTCcATCTATCCCGGCCATATA
3 DR1 306 tTCTCCCAGGCGCCACTGGACAACGCAAGACTGCAATTGTTCTATCTATCCCGGCCATATA
2 DK9 306 CTCCCCCAGaCGCCACTGGACAACGCAAGACTGCAACTGTTCTATCTACCCCGGCCATATt
6 S18 306 CTCCCCCAGGCGCCACTGGACAACGCAAGACTGCAACTGTTCTATCTACCCCGGCCATATA
7 SW1 306 CTCCCCCAGGCGCCACTGGACAACGCAAGACTGtAACTGTTCTATCTAtCCCGGCCAcATA
1-8 consensus cTCtCCCAGgCgCCaCTGGACaACGCAaGaCTGcAAtTGTTCtATCTAtCCcGGCCAtATa

FIGURE 1A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8 S11 367 ACGGGTCACCGCATGGCaTGGGATATGATGATGAACTGGTCCCCTACGgCGGCGTTGGTgG
4 DR4 367 ACGGGcCACCGCATGGCgTGGGATATGATGATGAACTGGTCCCCTACGACAGCGCTGGTAG
3 DR1 367 ACGGGaCACCGtATGGCaTGGGATATGATGATGAACTGGTCCCCTACGACAGCGCTGGTAA
2 DK9 367 ACGGGTCAtCGcATGGCgTGGGATATGATGATGAACTGGTCCCCTACAgCAGCGCTGGTAA
6 S18 367 ACGGGTCACCGtATGGCATGGGATATGATGATGAACTGGTCCCCTACAACgGCGtTGGTAA
7 SW1 367 ACGGGTCACCGcATGGCATGGGATATGATGATGAACTGGTCCCCcACAACaGCGcTGGTAg
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1 DK7 428 TAGCTCAGCTGCTCCGGATCCCgCAAGCCATCTTGGACATGATCGCTGGTGCTCACTGGGG
8 S11 428 TAGCTCAGCTGCTCCGGATCCCACAAGCCATCTTGGACATGATCGCTGGTGCTCACTGGGG
4 DR4 428 TAGCTCAGCTGCTCCGGATCCCACAAGCCATCTTGGACATGATCGCTGGTGCCCACTGGGG
3 DR1 428 TGGCTCAGCTGCTCCGGATCCCACAAGCCATCTTGGACATGATCGCTGGaGCCCACTGGGG
2 DK9 428 TGGCgCAGCTGCTCAGGATCCCGCAgGCCATCTTGGGACATGATCGCTGGTGCCCACTGGGG
6 S18 428 TAGCTCAGCTGCTCAGGgTCCCGCAAGCCGTCTTGGACATGATCGCTGGTGCCCACTGGGG
7 SW1 428 TAGCTCAGCTGCTCAGGaTCCCGCAAGCCGTCTTGGACATGATCGCTGGTGCCCACTGGGG
1-8 consensus TaGCtCAGCTGCTCcGGaTCCC-CAaGCCaTCTTGGAcATGATCGCTGGtGCcCACTGGGG
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6 S18 489 AGTCCTAGCGGGCATAGCGTATTTCTCCATGGcGGGGAACTGGGCGAAGGTCCTGcTAGTG
7 SW1 489 AGTCCTAGCGGGCATAGCGTATTTCTCCATGGtGGGGAACTGGGCGAAGGTCCTGaTAGTG
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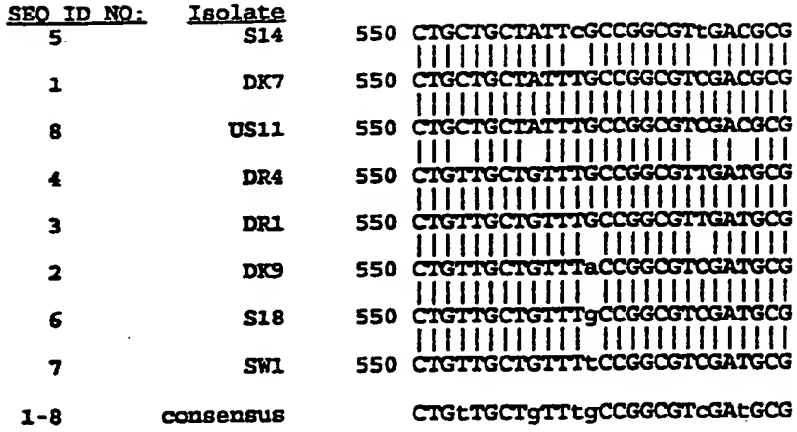
FIGURE 1A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6 S18 550 CTGTTGCTGTTTgCCGGCGTCGATGCG
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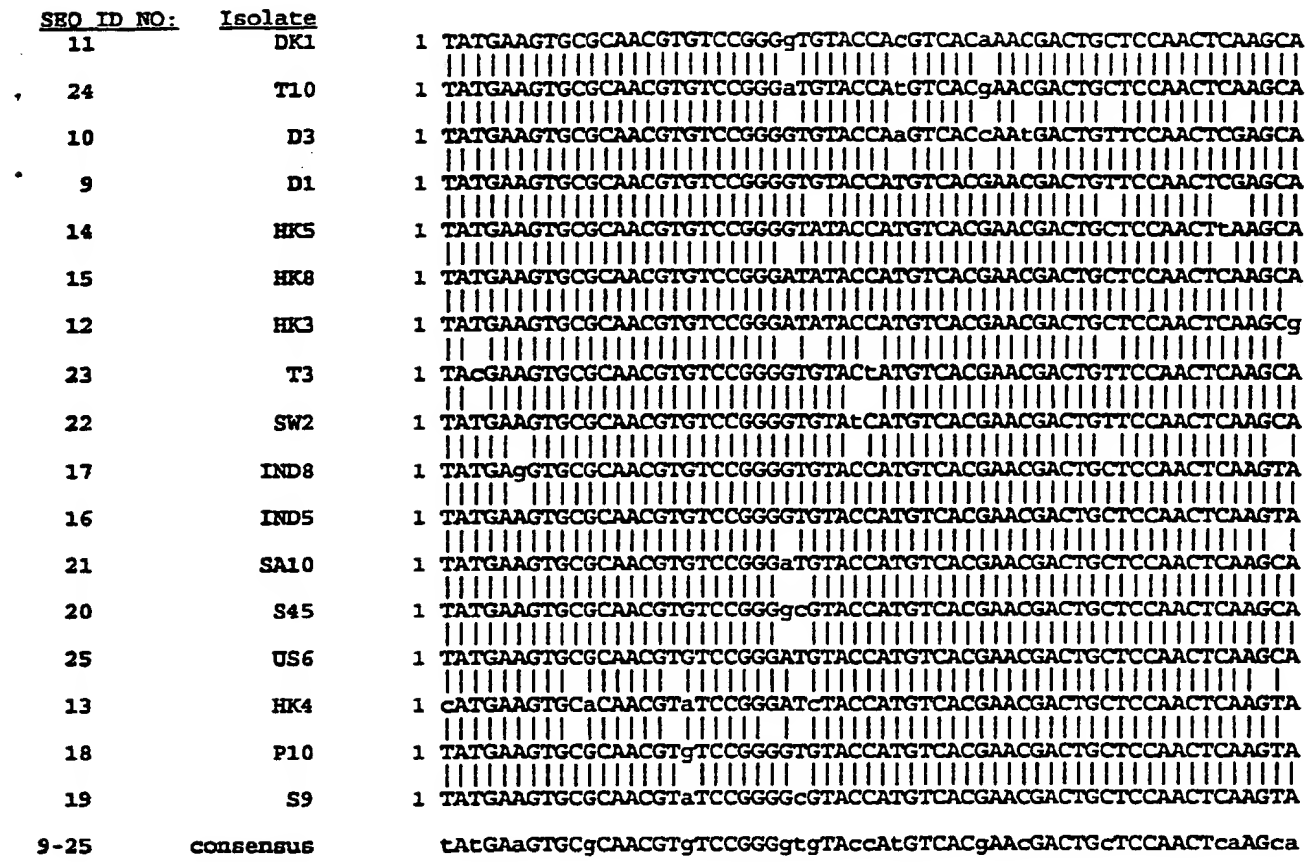
FIGURE 1B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10 D3 1 TATGAAGTGCGCAACGTGTCCGGGGTGTACCAaGTCACcAAtGACTGTTCCAACTCGAGCA
9 D1 1 TATGAAGTGCGCAACGTGTCCGGGGTGTACCATGTCACGAACGACTGTTCCAACTCGAGCA
14 HK5 1 TATGAAGTGCGCAACGTGTCCGGGGTATACCATGTCACGAACGACTGCTCCAACTtAAGCA
15 HK8 1 TATGAAGTGCGCAACGTGTCCGGGATATACCATGTCACGAACGACTGCTCCAACTCAAGCA
12 HK3 1 TATGAAGTGCGCAACGTGTCCGGGATATACCATGTCACGAACGACTGCTCCAACTCAAGCg
23 T3 1 TAcGAAGTGCGCAACGTGTCCGGGGTGTACtATGTCACGAACGACTGTTCCAACTCAAGCA
22 SW2 1 TATGAAGTGCGCAACGTGTCCGGGGTGTAtCATGTCACGAACGACTGTTCCAACTCAAGCA
17 IND8 1 TATGAgGTGCGCAACGTGTCCGGGGTGTACCATGTCACGAACGACTGCTCCAACTCAAGTA
16 IND5 1 TATGAAGTGCGCAACGTGTCCGGGGTGTACCATGTCACGAACGACTGCTCCAACTCAAGTA
21 SA10 1 TATGAAGTGCGCAACGTGTCCGGGaTGTACCATGTCACGAACGACTGCTCCAACTCAAGCA
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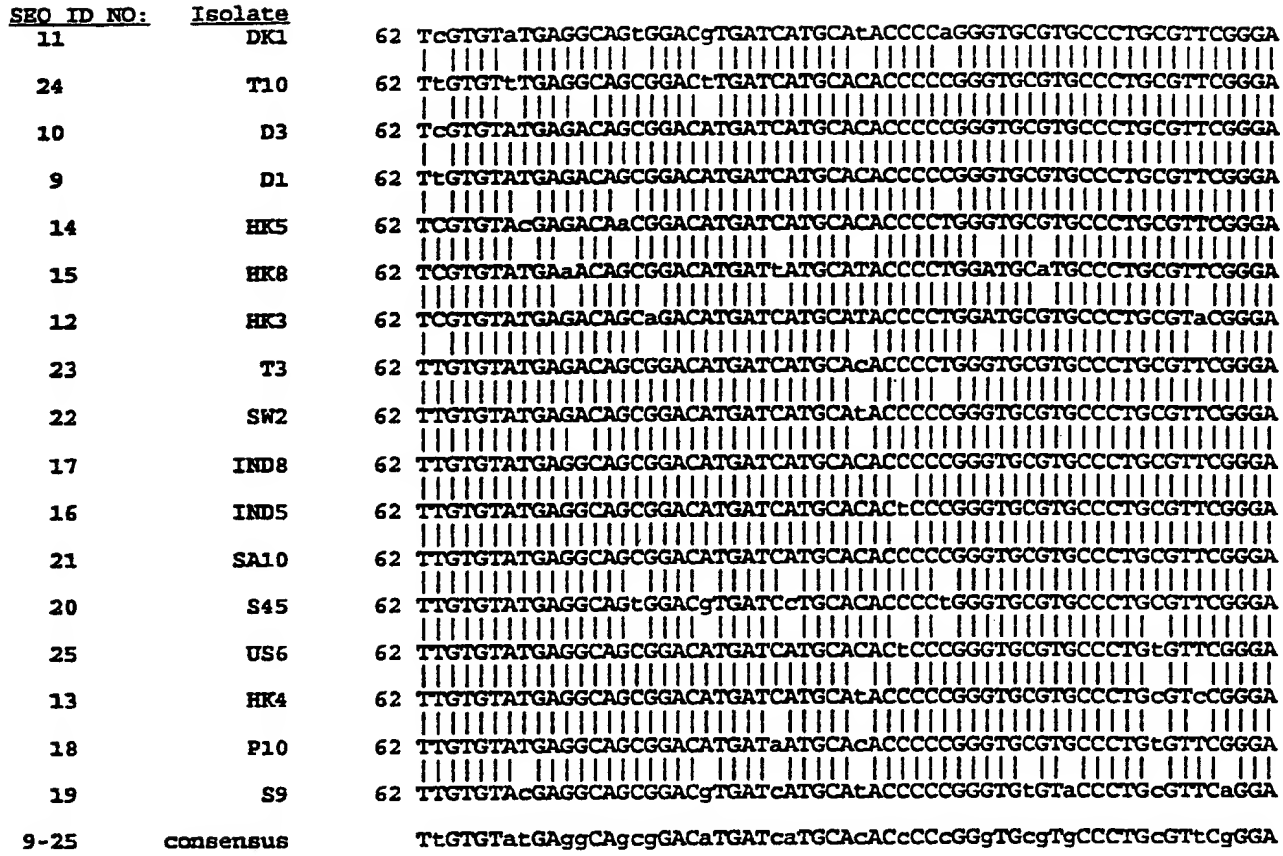
13 HK4 1 cATGAAGTGCaCAACGTaTCCGGGATcTACCATGTCACGAACGACTGCTCCAACTCAAGTA
18 P10 1 TATGAAGTGCGCAACGTgTCCGGGGTGTACCATGTCACGAACGACTGCTCCAACTCAAGTA
19 S9 1 TATGAAGTGCGCAACGTaTCCGGGGcGTACCATGTCACGAACGACTGCTCCAACTCAAGTA
9-25 consensus tAtGAaGTGCgCAACGTgTCCGGGgtgTAccAtGTCACgAAcGACTGcTCCAACTcaAGca

FIGURE 1B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10 D3 62 TcGTGTATGAGACAGCGGACATGATCATGCACACCCCCGGGTGCGTGCCCTGCGTTCGGGA
9 D1 62 TtGTGTATGAGACAGCGGACATGATCATGCACACCCCCGGGTGCGTGCCCTGCGTTCGGGA
14 HK5 62 TCGTGTAcGAGACAaCGGACATGATCATGCACACCCCTGGGTGCGTGCCCTGCGTTCGGGA
15 HK8 62 TCGTGTATGAaACAGCGGACATGATtATGCATACCCCTGGATGCaTGCCCTGCGTTCGGGA
12 HK3 62 TCGTGTATGAGACAGCaGACATGATCATGCATACCCCTGGATGCGTGCCCTGCGTaCGGGA
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17 IND8 62 TTGTGTATGAGGCAGCGGACATGATCATGCACACCCCCGGGTGCGTGCCCTGCGTTCGGGA
16 IND5 62 TTGTGTATGAGGCAGCGGACATGATCATGCACACtCCCGGGTGCGTGCCCTGCGTTCGGGA
21 SA10 62 TTGTGTATGAGGCAGCGGACATGATCATGCACACCCCCGGGTGCGTGCCCTGCGTTCGGGA
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13 HK4 62 TTGTGTATGAGGCAGCGGACATGATCATGCAtACCCCCGGGTGCGTGCCCTGcGTcCGGGA
18 P10 62 TTGTGTATGAGGCAGCGGACATGATaATGCAcACCCCCGGGTGCGTGCCCTGtGTTCGGGA
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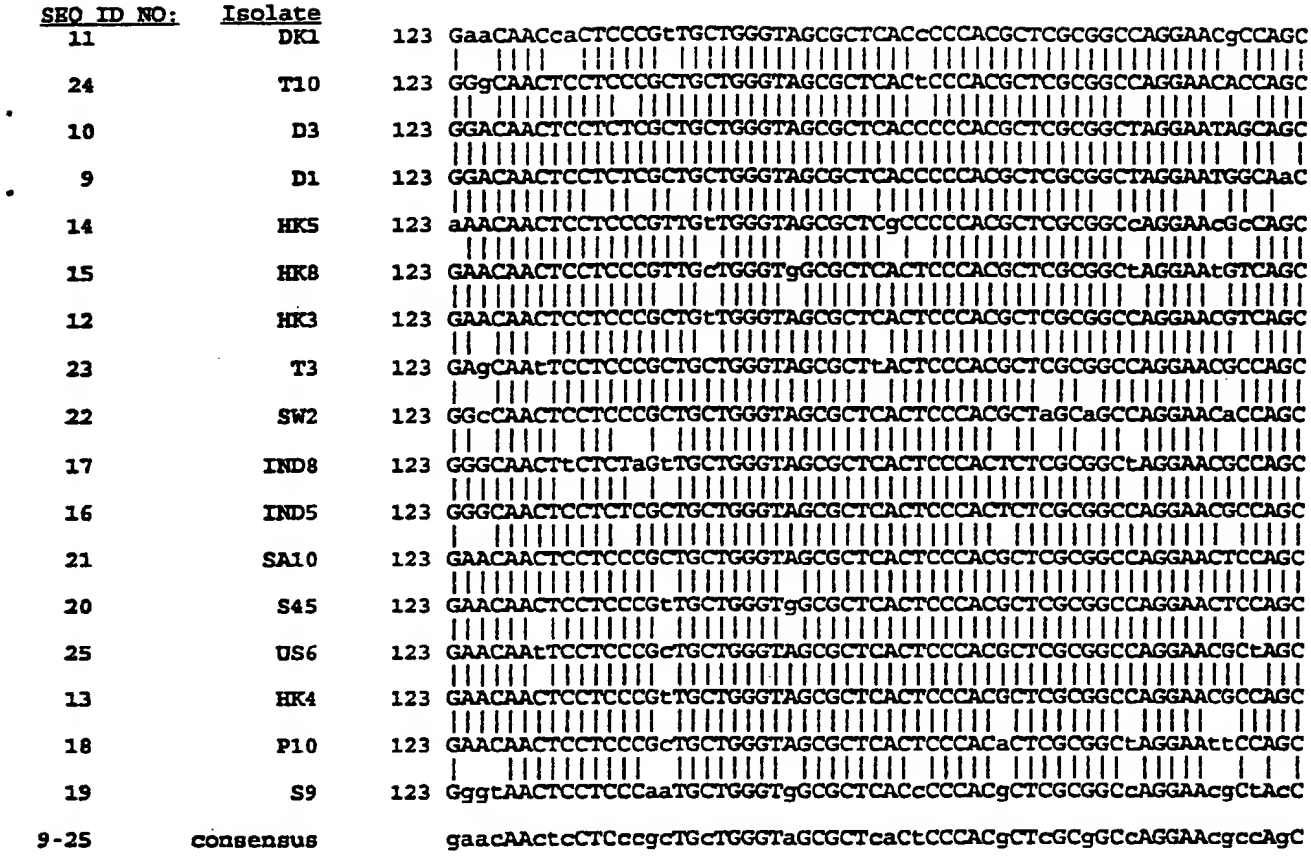
FIGURE 1B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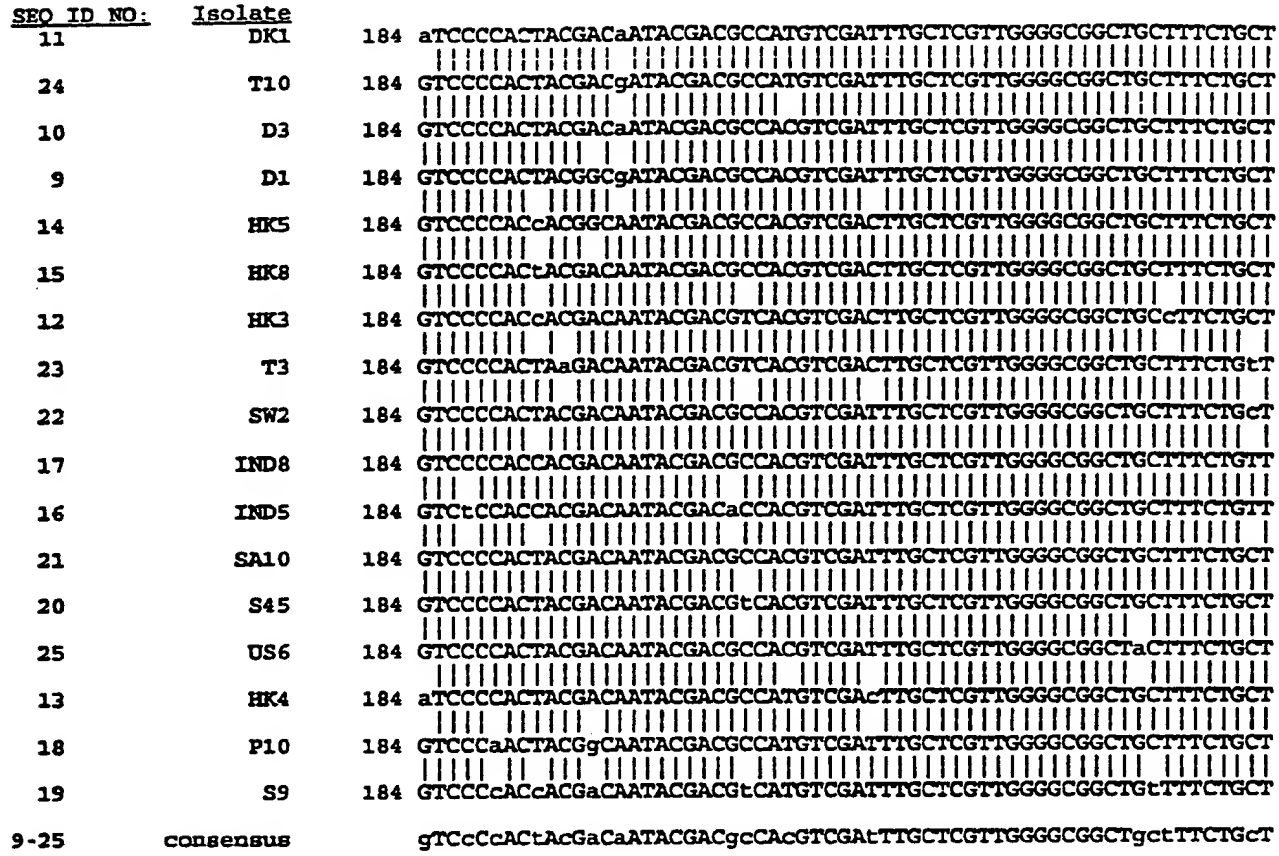
12 HK3 123 GAACAACTCCTCCCGCTGtTGGGTAGCGCTCACTCCCACGCTCGCGGCCAGGAACGTCAGC
23 T3 123 GAgCAAtTCCTCCCGCTGCTGGGTAGCGCTtACTCCCACGCTCGCGGCCAGGAACGCCAGC
22 SW2 123 GGcCAACTCCTCCCGCTGCTGGGTAGCGCTCACTCCCACGCTaGCaGCCAGGAACaCCAGC
17 IND8 123 GGGCAACTtCTCTaGtTGCTGGGTAGCGCTCACTCCCACTCTCGCGGCtAGGAACGCCAGC
16 IND5 123 GGGCAACTCCTCTCGCTGCTGGGTAGCGCTCACTCCCACTCTCGCGGCCAGGAACGCCAGC
21 SA10 123 GAACAACTCCTCCCGCTGCTGGGTAGCGCTCACTCCCACGCTCGCGGCCAGGAACTCCAGC
20 S45 123 GAACAACTCCTCCCGtTGCTGGGTgGCGCTCACTCCCACGCTCGCGGCCAGGAACTCCAGC
25 US6 123 GAACAAtTCCTCCCGcTGCTGGGTAGCGCTCACTCCCACGCTCGCGGCCAGGAACGCtAGC
13 HK4 123 GAACAACTCCTCCCGtTGCTGGGTAGCGCTCACTCCCACGCTCGCGGCCAGGAACGCCAGC
18 P10 123 GAACAACTCCTCCCGcTGCTGGGTAGCGCTCACTCCCACaCTCGCGGCtAGGAAttCCAGC
19 S9 123 GggtAACTCCTCCCaaTGCTGGGTgGCGCTCACcCCCACgCTCGCGGCcAGGAAcgCtAcC
9-25 consensus gaacAActcCTCccgcTGcTGGGTaGCGCTcaCtCCCACgCTcGCgGCcAGGAAcgccAgC

FIGURE 1B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10 D3 184 GTCCCCACTACGACaATACGACGCCACGTCGATTTGCTCGTTGGGGCGGCTGCTTTCTGCT
9 D1 184 GTCCCCACTACGGCgATACGACGCCACGTCGATTTGCTCGTTGGGGCGGCTGCTTTCTGCT
14 HK5 184 GTCCCCACcACGGCAATACGACGCCACGTCGACTTGCTCGTTGGGGCGGCTGCTTTCTGCT
15 HK8 184 GTCCCCACtACGACAATACGACGCCACGTCGACTTGCTCGTTGGGGCGGCTGCTTTCTGCT
12 HK3 184 GTCCCCACcACGACAATACGACGTCACGTCGACTTGCTCGTTGGGGCGGCTGCcTTCTGCT
23 T3 184 GTCCCCACTAaGACAATACGACGTCACGTCGACTTGCTCGTTGGGGCGGCTGCTTTCTGtT
22 SW2 184 GTCCCCACTACGACAATACGACGCCACGTCGATTTGCTCGTTGGGGCGGCTGCTTTCTGcT
17 IND8 184 GTCCCCACCACGACAATACGACGCCACGTCGATTTGCTCGTTGGGGCGGCTGCTTTCTGTT
16 IND5 184 GTCtCCACCACGACAATACGACaCCACGTCGATTTGCTCGTTGGGGCGGCTGCTTTCTGTT
21 SA10 184 GTCCCCACTACGACAATACGACGCCACGTCGATTTGCTCGTTGGGGCGGCTGCTTTCTGCT
20 S45 184 GTCCCCACTACGACAATACGACGtCACGTCGATTTGCTCGTTGGGGCGGCTGCTTTCTGCT
25 US6 184 GTCCCCACTACGACAATACGACGCCACGTCGATTTGCTCGTTGGGGCGGCTaCTTTCTGCT
13 HK4 184 aTCCCCACTACGACAATACGACGCCATGTCGAcTTGCTCGTTGGGGCGGCTGCTTTCTGCT
18 P10 184 GTCCCaACTACGgCAATACGACGCCATGTCGATTTGCTCGTTGGGGCGGCTGCTTTCTGCT
19 S9 184 GTCCCcACcACGaCAATACGACGtCATGTCGATTTGCTCGTTGGGGCGGCTGtTTTCTGCT
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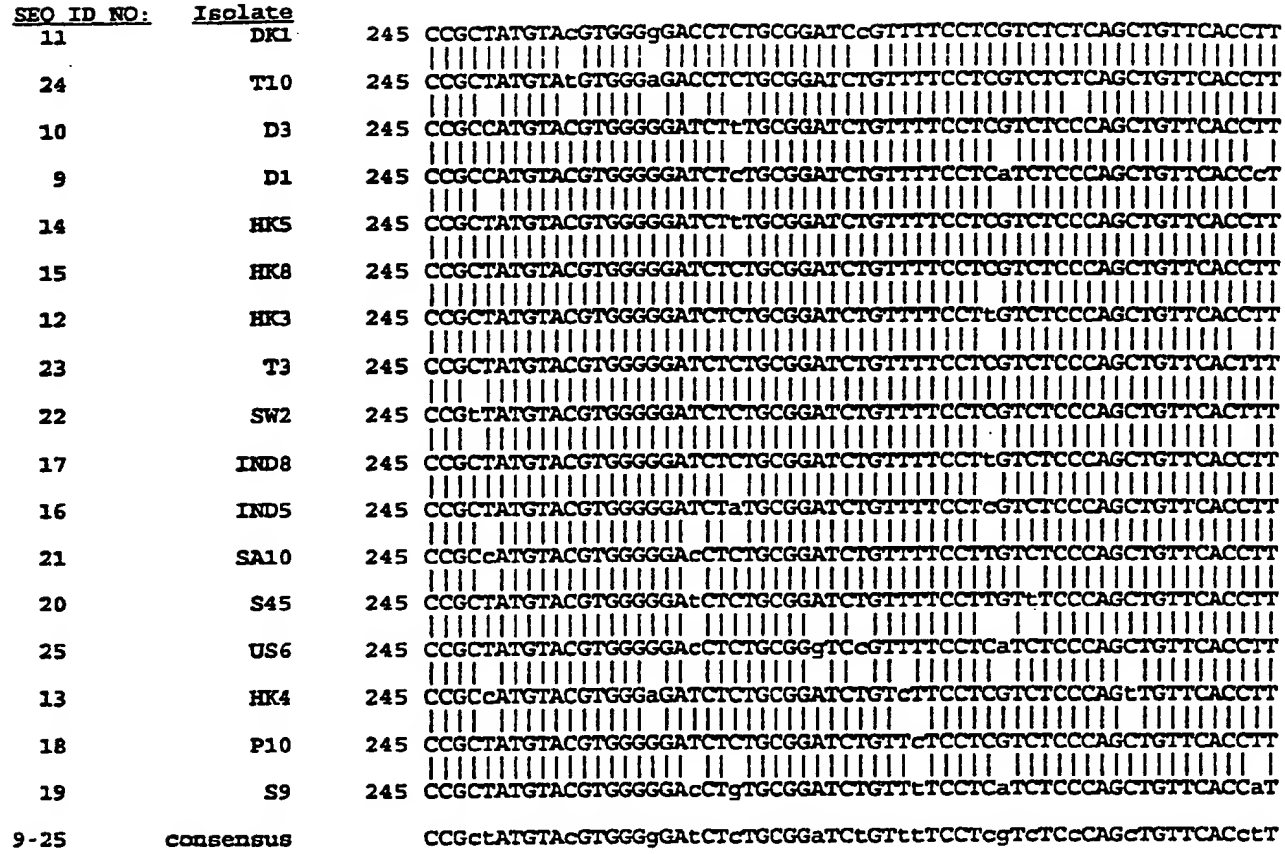
FIGURE 1B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10 D3 245 CCGCCATGTACGTGGGGGATCTtTGCGGATCTGTTTTCCTCGTCTCCCAGCTGTTCACCTT
9 D1 245 CCGCCATGTACGTGGGGGATCTcTGCGGATCTGTTTTCCTCaTCTCCCAGCTGTTCACCcT
14 HK5 245 CCGCTATGTACGTGGGGGATCTtTGCGGATCTGTTTTCCTCGTCTCCCAGCTGTTCACCTT
15 HK8 245 CCGCTATGTACGTGGGGGATCTCTGCGGATCTGTTTTCCTCGTCTCCCAGCTGTTCACCTT
12 HK3 245 CCGCTATGTACGTGGGGGATCTCTGCGGATCTGTTTTCCTtGTCTCCCAGCTGTTCACCTT
23 T3 245 CCGCTATGTACGTGGGGGATCTCTGCGGATCTGTTTTCCTCGTCTCCCAGCTGTTCACTTT
22 SW2 245 CCGtTATGTACGTGGGGGATCTCTGCGGATCTGTTTTCCTCGTCTCCCAGCTGTTCACTTT
17 IND8 245 CCGCTATGTACGTGGGGGATCTCTGCGGATCTGTTTTCCTtGTCTCCCAGCTGTTCACCTT
16 IND5 245 CCGCTATGTACGTGGGGGATCTaTGCGGATCTGTTTTCCTcGTCTCCCAGCTGTTCACCTT
21 SA10 245 CCGCcATGTACGTGGGGGAcCTCTGCGGATCTGTTTTCCTTGTCTCCCAGCTGTTCACCTT
20 S45 245 CCGCTATGTACGTGGGGGAtCTCTGCGGATCTGTTTTCCTTGTtTCCCAGCTGTTCACCTT
25 US6 245 CCGCTATGTACGTGGGGGAcCTCTGCGGgTCcGTTTTCCTCaTCTCCCAGCTGTTCACCTT
13 HK4 245 CCGCcATGTACGTGGGaGATCTCTGCGGATCTGTcTTCCTCGTCTCCCAGtTGTTCACCTT
18 P10 245 CCGCTATGTACGTGGGGGATCTCTGCGGATCTGTTcTCCTCGTCTCCCAGCTGTTCACCTT
19 S9 245 CCGCTATGTACGTGGGGGAcCTgTGCGGATCTGTTtTCCTCaTCTCCCAGCTGTTCACCaT
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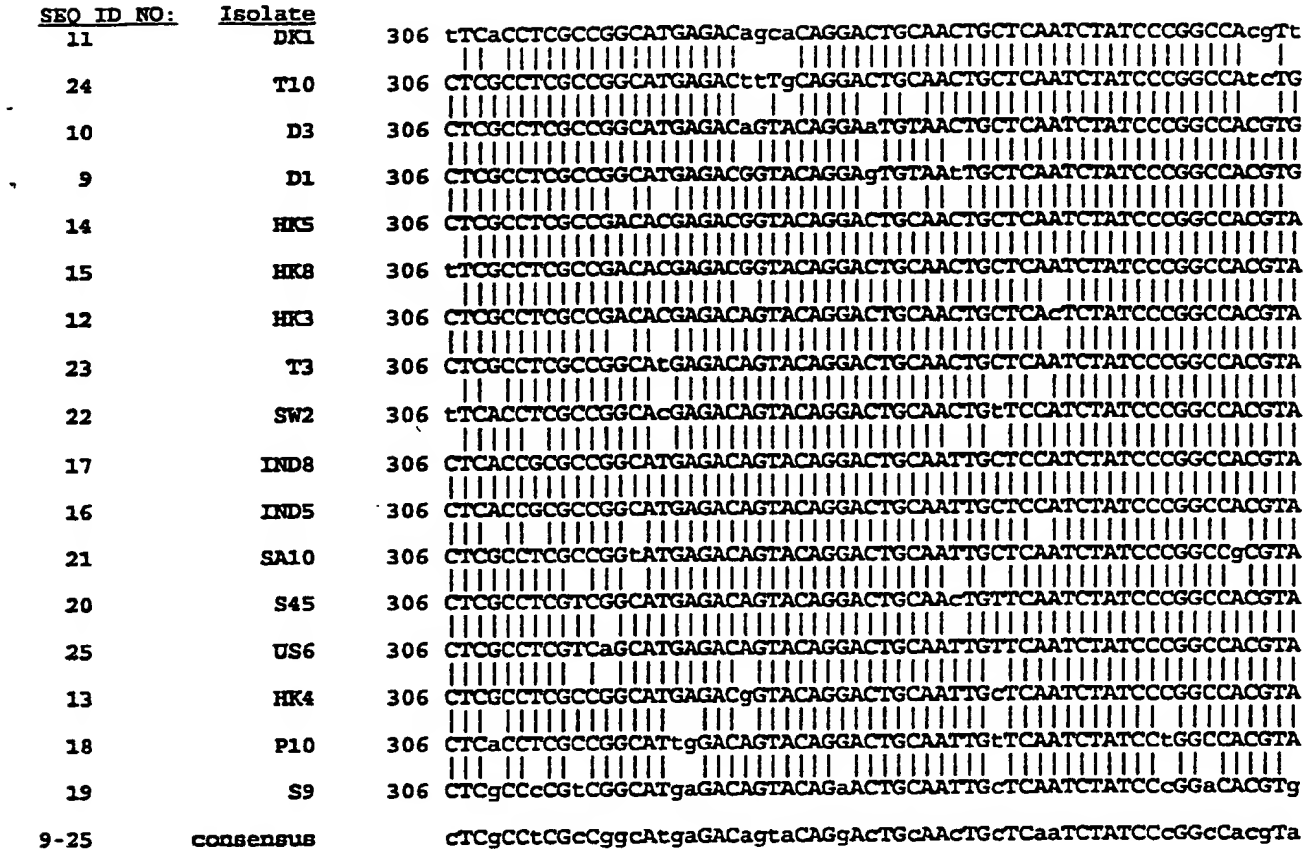
FIGURE 1B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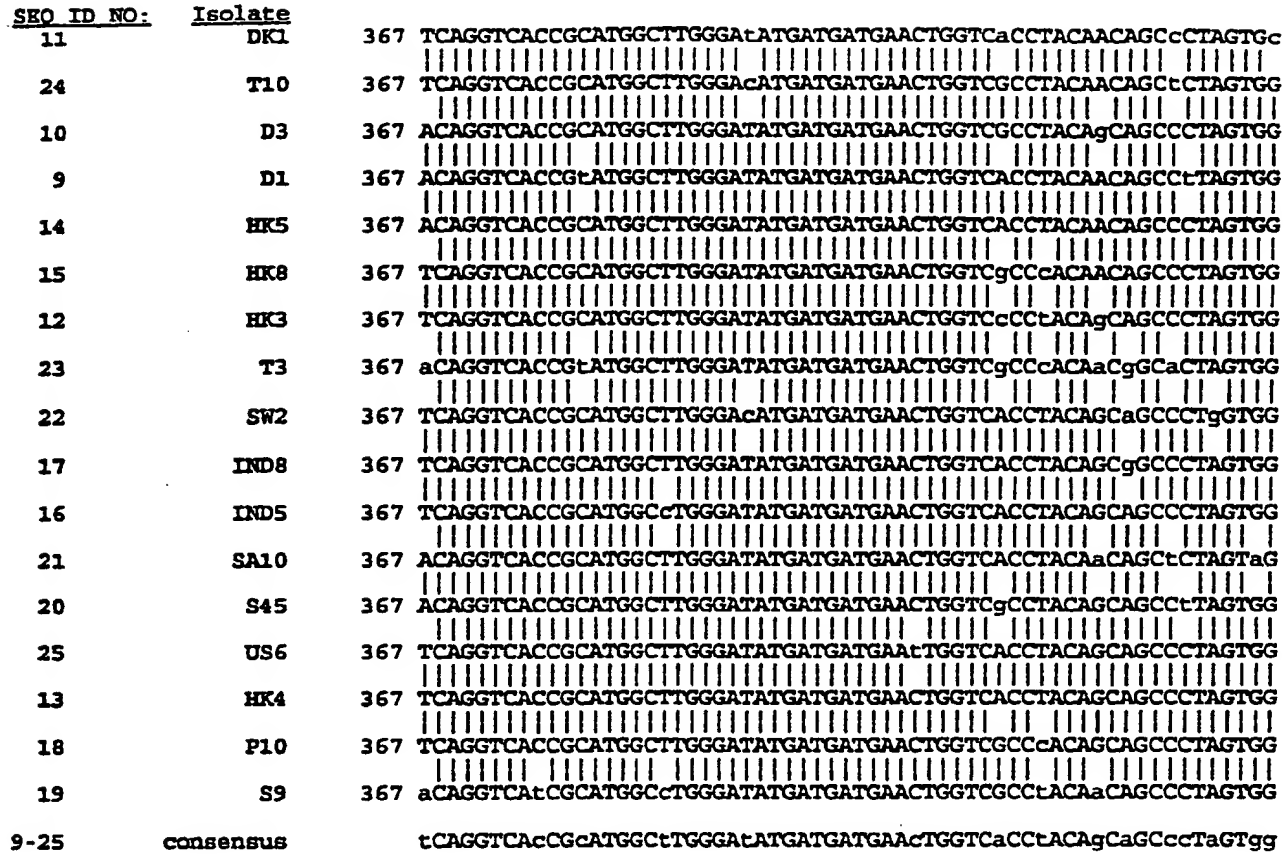
10 D3 306 CTCGCCTCGCCGGCATGAGACaGTACAGGAaTGTAACTGCTCAATCTATCCCGGCCACGTG
9 D1 306 CTCGCCTCGCCGGCATGAGACGGTACAGGAgTGTAAtTGCTCAATCTATCCCGGCCACGTG
14 HK5 306 CTCGCCTCGCCGACACGAGACGGTACAGGACTGCAACTGCTCAATCTATCCCGGCCACGTA
15 HK8 306 tTCGCCTCGCCGACACGAGACGGTACAGGACTGCAACTGCTCAATCTATCCCGGCCACGTA
12 HK3 306 CTCGCCTCGCCGACACGAGACAGTACAGGACTGCAACTGCTCAcTCTATCCCGGCCACGTA
23 T3 306 CTCGCCTCGCCGGCAtGAGACAGTACAGGACTGCAACTGCTCAATCTATCCCGGCCACGTA
22 SW2 306 tTCACCTCGCCGGCAcGAGACAGTACAGGACTGCAACTGtTCCATCTATCCCGGCCACGTA
17 IND8 306 CTCACCGCGCCGGCATGAGACAGTACAGGACTGCAATTGCTCCATCTATCCCGGCCACGTA
16 IND5 306 CTCACCGCGCCGGCATGAGACAGTACAGGACTGCAATTGCTCCATCTATCCCGGCCACGTA
21 SA10 306 CTCGCCTCGCCGGtATGAGACAGTACAGGACTGCAATTGCTCAATCTATCCCGGCCgCGTA
20 S45 306 CTCGCCTCGTCGGCATGAGACAGTACAGGACTGCAAcTGTTCAATCTATCCCGGCCACGTA
25 US6 306 CTCGCCTCGTCaGCATGAGACAGTACAGGACTGCAATTGTTCAATCTATCCCGGCCACGTA
13 HK4 306 CTCGCCTCGCCGGCATGAGACgGTACAGGACTGCAATTGcTCAATCTATCCCGGCCACGTA
18 P10 306 CTCaCCTCGCCGGCATtgGACAGTACAGGACTGCAATTGtTCAATCTATCCtGGCCACGTA
19 S9 306 CTCgCCcCGtCGGCATgaGACAGTACAGaACTGCAATTGcTCAATCTATCCcGGaCACGTg
9-25 consensus cTCgCCtCGcCggcAtgaGACagtaCAGgAcTGcAAcTGcTCaaTCTATCCcGGcCacgTa

FIGURE 1B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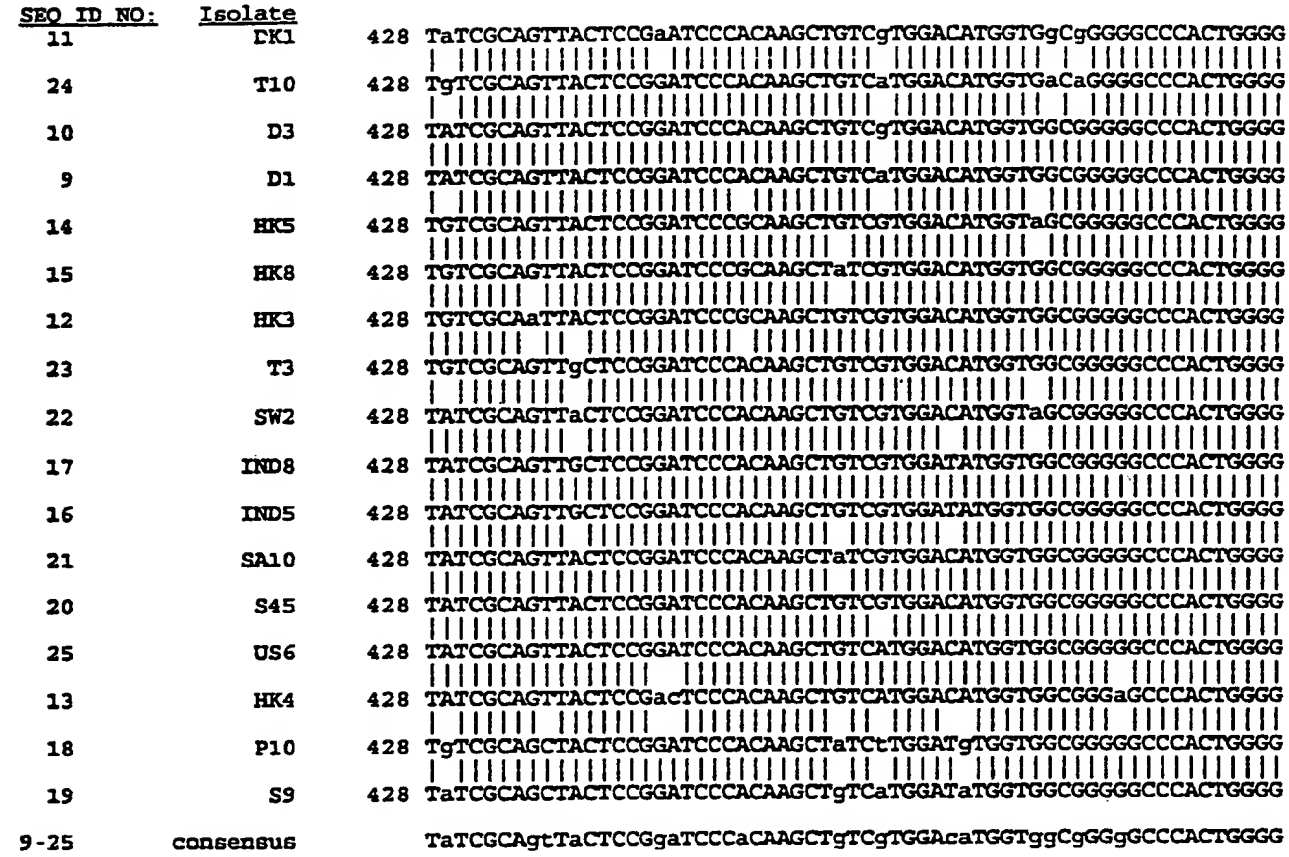
10 D3 367 ACAGGTCACCGCATGGCTTGGGATATGATGATGAACTGGTCGCCTACAgCAGCCCTAGTGG
9 D1 367 ACAGGTCACCGtATGGCTTGGGATATGATGATGAACTGGTCACCTACAACAGCCtTAGTGG
14 HK5 367 ACAGGTCACCGCATGGCTTGGGATATGATGATGAACTGGTCACCTACAACAGCCCTAGTGG
15 HK8 367 TCAGGTCACCGCATGGCTTGGGATATGATGATGAACTGGTCgCCcACAACAGCCCTAGTGG
12 HK3 367 TCAGGTCACCGCATGGCTTGGGATATGATGATGAACTGGTCcCCtACAgCAGCCCTAGTGG
23 T3 367 aCAGGTCACCGtATGGCTTGGGATATGATGATGAACTGGTCgCCcACAaCgGCaCTAGTGG
22 SW2 367 TCAGGTCACCGCATGGCTTGGGAcATGATGATGAACTGGTCACCTACAGCaGCCCTgGTGG
17 IND8 367 TCAGGTCACCGCATGGCTTGGGATATGATGATGAACTGGTCACCTACAGCgGCCCTAGTGG
16 IND5 367 TCAGGTCACCGCATGGCcTGGGATATGATGATGAACTGGTCACCTACAGCAGCCCTAGTGG
21 SA10 367 ACAGGTCACCGCATGGCTTGGGATATGATGATGAACTGGTCACCTACAaCAGCtCTAGTaG
20 S45 367 ACAGGTCACCGCATGGCTTGGGATATGATGATGAACTGGTCgCCTACAGCAGCCtTAGTGG
25 US6 367 TCAGGTCACCGCATGGCTTGGGATATGATGATGAAtTGGTCACCTACAGCAGCCCTAGTGG
13 HK4 367 TCAGGTCACCGCATGGCTTGGGATATGATGATGAACTGGTCACCTACAGCAGCCCTAGTGG
18 P10 367 TCAGGTCACCGCATGGCTTGGGATATGATGATGAACTGGTCGCCcACAGCAGCCCTAGTGG
19 S9 367 aCAGGTCAtCGCATGGCcTGGGATATGATGATGAACTGGTCGCCtACAaCAGCCCTAGTGG
9-25 consensus tCAGGTCAcCGcATGGCtTGGGAtATGATGATGAAcTGGTCaCCtACAgCaGCccTaGTgg

FIGURE 1B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10 D3 428 TATCGCAGTTACTCCGGATCCCACAAGCTGTCgTGGACATGGTGGCGGGGGCCCACTGGGG
9 D1 428 TATCGCAGTTACTCCGGATCCCACAAGCTGTCaTGGACATGGTGGCGGGGGCCCACTGGGG
14 HK5 428 TGTCGCAGTTACTCCGGATCCCGCAAGCTGTCGTGGACATGGTaGCGGGGGCCCACTGGGG
15 HK8 428 TGTCGCAGTTACTCCGGATCCCGCAAGCTaTCGTGGACATGGTGGCGGGGGCCCACTGGGG
12 HK3 428 TGTCGCAaTTACTCCGGATCCCGCAAGCTGTCGTGGACATGGTGGCGGGGGCCCACTGGGG
23 T3 428 TGTCGCAGTTgCTCCGGATCCCACAAGCTGTCGTGGACATGGTGGCGGGGGCCCACTGGGG
22 SW2 428 TATCGCAGTTaCTCCGGATCCCACAAGCTGTCGTGGACATGGTaGCGGGGGCCCACTGGGG
17 IND8 428 TATCGCAGTTGCTCCGGATCCCACAAGCTGTCGTGGATATGGTGGCGGGGGCCCACTGGGG
16 IND5 428 TATCGCAGTTGCTCCGGATCCCACAAGCTGTCGTGGATATGGTGGCGGGGGCCCACTGGGG
21 SA10 428 TATCGCAGTTACTCCGGATCCCACAAGCTaTCGTGGACATGGTGGCGGGGGCCCACTGGGG
20 S45 428 TATCGCAGTTACTCCGGATCCCACAAGCTGTCGTGGACATGGTGGCGGGGGCCCACTGGGG
25 US6 428 TATCGCAGTTACTCCGGATCCCACAAGCTGTCATGGACATGGTGGCGGGGGCCCACTGGGG
13 HK4 428 TATCGCAGTTACTCCGacTCCCACAAGCTGTCATGGACATGGTGGCGGGaGCCCACTGGGG
18 P10 428 TgTCGCAGCTACTCCGGATCCCACAAGCTaTCtTGGATgTGGTGGCGGGGGCCCACTGGGG
19 S9 428 TaTCGCAGCTACTCCGGATCCCACAAGCTgTCaTGGATaTGGTGGCGGGGGCCCACTGGGG
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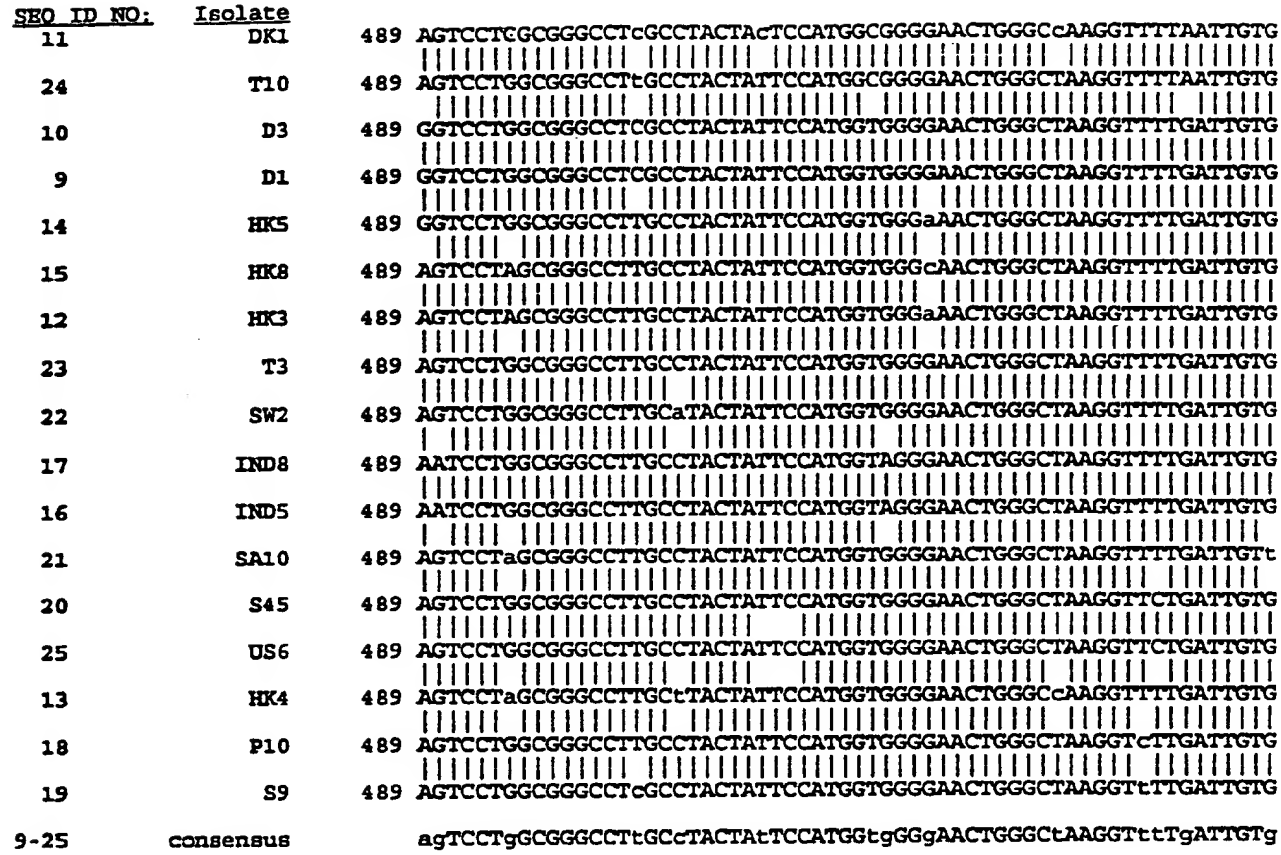
FIGURE 1B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10 D3 489 GGTCCTGGCGGGCCTCGCCTACTATTCCATGGTGGGGAACTGGGCTAAGGTTTTGATTGTG
9 D1 489 GGTCCTGGCGGGCCTCGCCTACTATTCCATGGTGGGGAACTGGGCTAAGGTTTTGATTGTG
14 HK5 489 GGTCCTGGCGGGCCTTGCCTACTATTCCATGGTGGGaAACTGGGCTAAGGTTTTGATTGTG
15 HK8 489 AGTCCTAGCGGGCCTTGCCTACTATTCCATGGTGGGcAACTGGGCTAAGGTTTTGATTGTG
12 HK3 489 AGTCCTAGCGGGCCTTGCCTACTATTCCATGGTGGGaAACTGGGCTAAGGTTTTGATTGTG
23 T3 489 AGTCCTGGCGGGCCTTGCCTACTATTCCATGGTGGGGAACTGGGCTAAGGTTTTGATTGTG
22 SW2 489 AGTCCTGGCGGGCCTTGCaTACTATTCCATGGTGGGGAACTGGGCTAAGGTTTTGATTGTG
17 IND8 489 AATCCTGGCGGGCCTTGCCTACTATTCCATGGTAGGGAACTGGGCTAAGGTTTTGATTGTG
16 IND5 489 AATCCTGGCGGGCCTTGCCTACTATTCCATGGTAGGGAACTGGGCTAAGGTTTTGATTGTG
21 SA10 489 AGTCCTaGCGGGCCTTGCCTACTATTCCATGGTGGGGAACTGGGCTAAGGTTTTGATTGTt
20 S45 489 AGTCCTGGCGGGCCTTGCCTACTATTCCATGGTGGGGAACTGGGCTAAGGTTCTGATTGTG
25 US6 489 AGTCCTGGCGGGCCTTGCCTACTATTCCATGGTGGGGAACTGGGCTAAGGTTCTGATTGTG
13 HK4 489 AGTCCTaGCGGGCCTTGCtTACTATTCCATGGTGGGGAACTGGGCcAAGGTTTTGATTGTG
18 P10 489 AGTCCTGGCGGGCCTTGCCTACTATTCCATGGTGGGGAACTGGGCTAAGGTcTTGATTGTG
19 S9 489 AGTCCTGGCGGGCCTcGCCTACTATTCCATGGTGGGGAACTGGGCTAAGGTtTTGATTGTG
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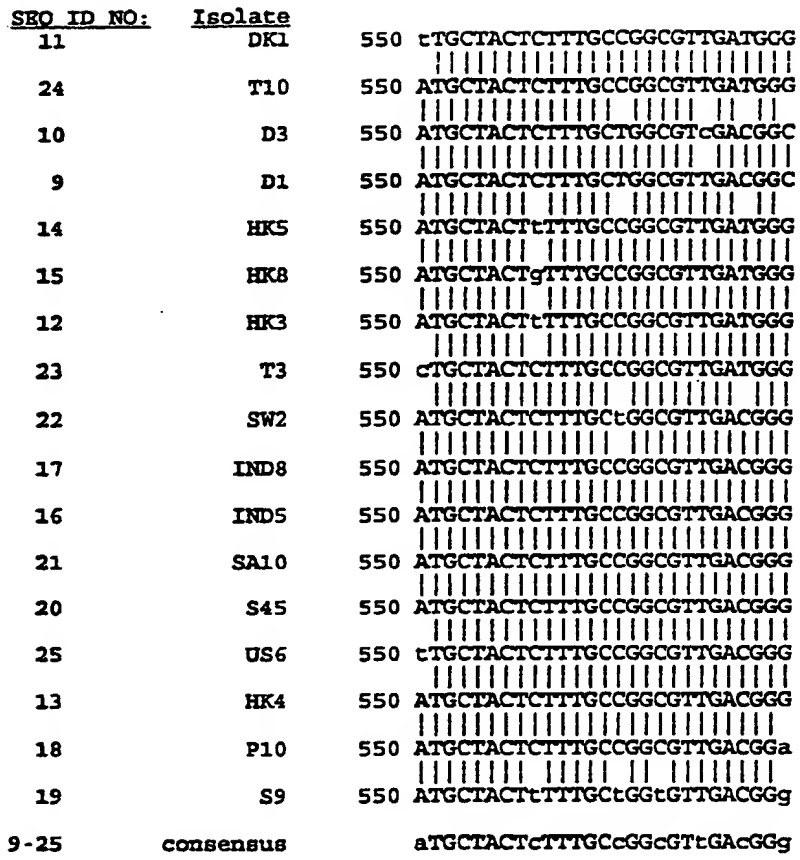
FIGURE 1B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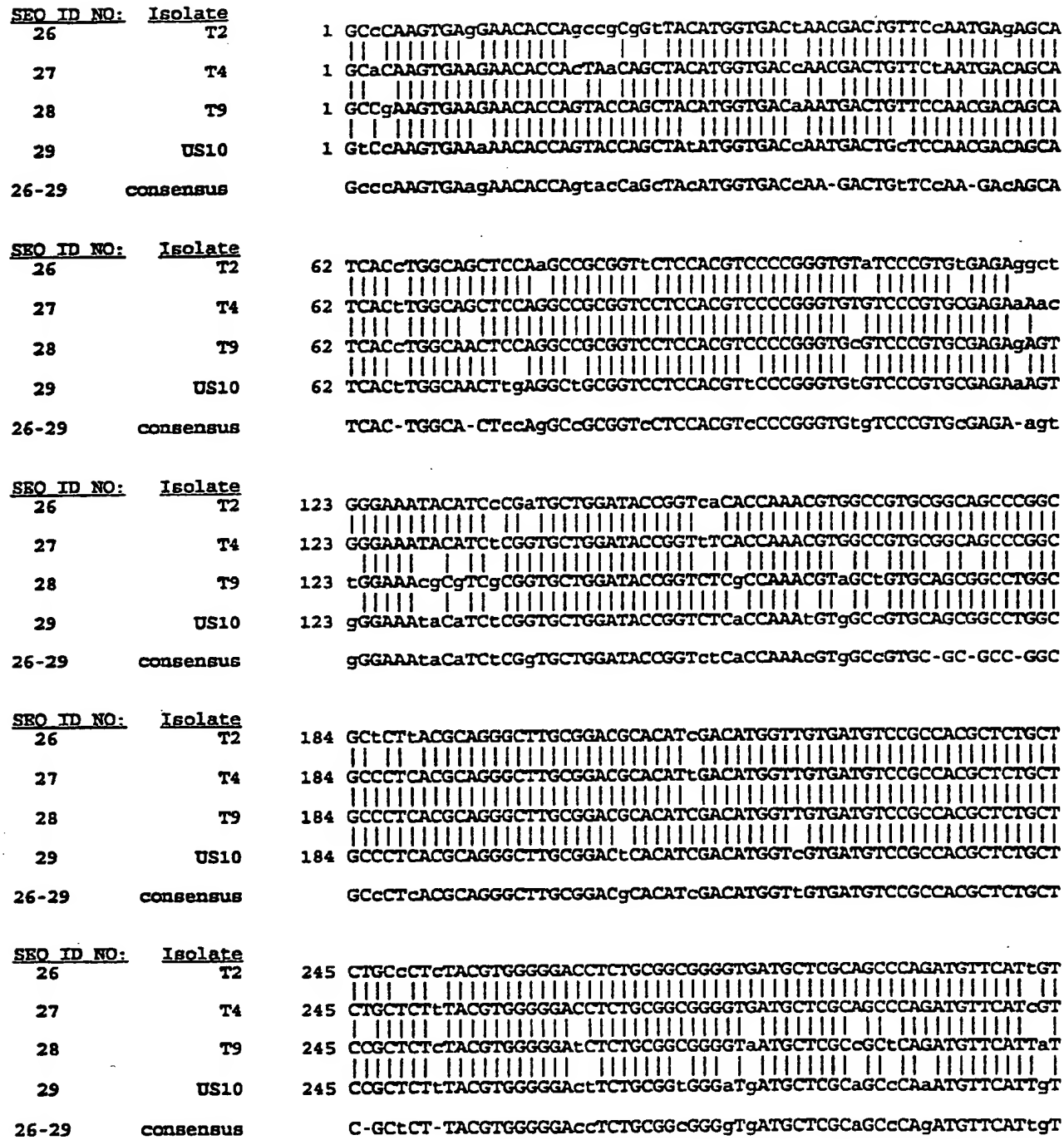
9 D1 550 ATGCTACTCTTTGCTGGCGTTGACGGC
14 HK5 550 ATGCTACTtTTTGCCGGCGTTGATGGG
15 HK8 550 ATGCTACTgTTTGCCGGCGTTGATGGG
12 HK3 550 ATGCTACTtTTTGCCGGCGTTGATGGG
23 T3 550 cTGCTACTCTTTGCCGGCGTTGATGGG
22 SW2 550 ATGCTACTCTTTGCtGGCGTTGACGGG
17 IND8 550 ATGCTACTCTTTGCCGGCGTTGACGGG
16 IND5 550 ATGCTACTCTTTGCCGGCGTTGACGGG
21 SA10 550 ATGCTACTCTTTGCCGGCGTTGACGGG
20 S45 550 ATGCTACTCTTTGCCGGCGTTGACGGG
25 US6 550 tTGCTACTCTTTGCCGGCGTTGACGGG
13 HK4 550 ATGCTACTCTTTGCCGGCGTTGACGGG
18 P10 550 ATGCTACTCTTTGCCGGCGTTGACGGa
19 S9 550 ATGCTACTtTTTGCtGGtGTTGACGGg
9-25 consensus aTGCTACTcTTTGCcGGcGTtGAcGGg

FIGURE 1C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28 T9 1 GCCgAAGTGAAGAACACCAGTACCAGCTACATGGTGACaAATGACTGTTCCAACGACAGCA
29 US10 1 GtCcAAGTGAAaAACACCAGTACCAGCTAtATGGTGACcAATGACTGcTCCAACGACAGCA
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27 T4 62 TCACtTGGCAGCTCCAGGCCGCGGTCCTCCACGTCCCCGGGTGTGTCCCGTGCGAGAaAac
28 T9 62 TCACcTGGCAACTCCAGGCCGCGGTCCTCCACGTCCCCGGGTGcGTCCCGTGCGAGAgAGT
29 US10 62 TCACtTGGCAACTtgAGGCtGCGGTCCTCCACGTtCCCGGGTGtGTCCCGTGCGAGAaAGT
26-29 consensus TCAC-TGGCA-CTccAgGCcGCGGTcCTCCACGTcCCCGGGTGtgTCCCGTGcGAGA-agt
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27 T4 123 GGGAAATACATCtCGGTGCTGGATACCGGTtTCACCAAACGTGGCCGTGCGGCAGCCCGGC
28 T9 123 tGGAAAcgCgTCgCGGTGCTGGATACCGGTCTCgCCAAACGTaGCtGTGCAGCGGCCTGGC
29 US10 123 gGGAAAtaCaTCtCGGTGCTGGATACCGGTCTCaCCAAAtGTgGCcGTGCAGCGGCCTGGC
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27 T4 184 GCCCTCACGCAGGGCTTGCGGACGCACATtGACATGGTTGTGATGTCCGCCACGCTCTGCT
28 T9 184 GCCCTCACGCAGGGCTTGCGGACGCACATCGACATGGTTGTGATGTCCGCCACGCTCTGCT
29 US10 184 GCCCTCACGCAGGGCTTGCGGACtCACATCGACATGGTcGTGATGTCCGCCACGCTCTGCT
26-29 consensus GCcCTcACGCAGGGCTTGCGGACgCACATcGACATGGTtGTGATGTCCGCCACGCTCTGCT
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27 T4 245 CTGCTCTtTACGTGGGGGACCTCTGCGGCGGGGTGATGCTCGCAGCCCAGATGTTCATcGT
28 T9 245 CCGCTCTcTACGTGGGGGAtCTCTGCGGCGGGGTaATGCTCGCcGCtCAGATGTTCATTaT
29 US10 245 CCGCTCTtTACGTGGGGGActTCTGCGGtGGGaTgATGCTCGCaGCcCAaATGTTCATTgT
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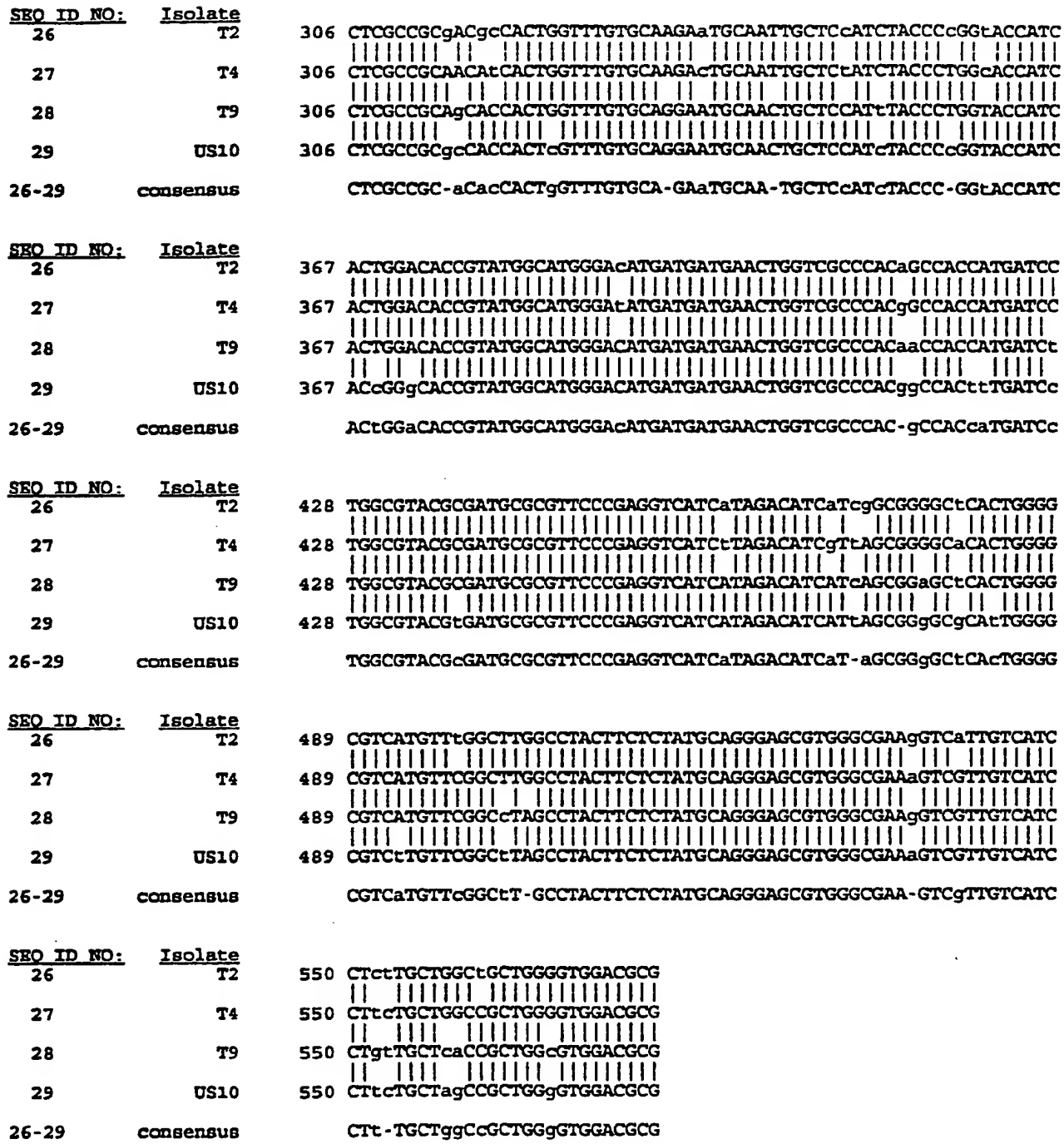
FIGURE 1C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28 T9 367 ACTGGACACCGTATGGCATGGGACATGATGATGAACTGGTCGCCCACaaCCACCATGATCt
29 US10 367 ACcGGgCACCGTATGGCATGGGACATGATGATGAACTGGTCGCCCACggCCACttTGATCc
26-29 consensus ACtGGaCACCGTATGGCATGGGAcATGATGATGAACTGGTCGCCCAC-gCCACcaTGATCc
SEQ ID NO: Isolate
26 T2 428 TGGCGTACGCGATGCGCGTTCCCGAGGTCATCaTAGACATCaTcgGCGGGGCtCACTGGGG
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29 US10 428 TGGCGTACGtGATGCGCGTTCCCGAGGTCATCATAGACATCATtAGCGGgGCgCAtTGGGG
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SEQ ID NO: Isolate
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28 T9 489 CGTCATGTTCGGCcTAGCCTACTTCTCTATGCAGGGAGCGTGGGCGAAgGTCGTTGTCATC
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26-29 consensus CGTCaTGTTcGGCtT-GCCTACTTCTCTATGCAGGGAGCGTGGGCGAA-GTCgTTGTCATC
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26 T2 550 CTctTGCTGGCtGCTGGGGTGGACGCG
27 T4 550 CTtcTGCTGGCCGCTGGGGTGGACGCG
28 T9 550 CTgtTGCTcaCCGCTGGcGTGGACGCG
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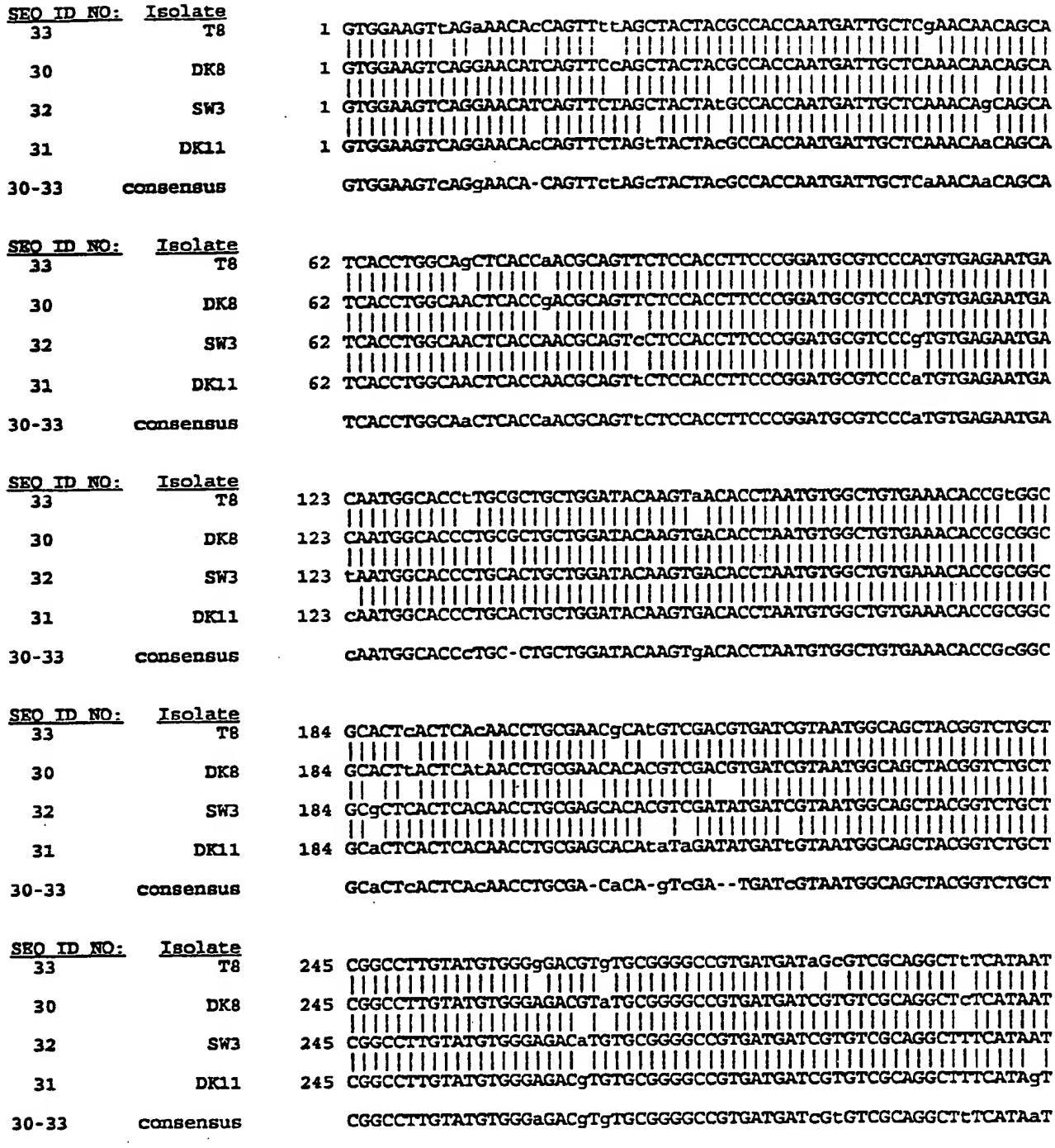
FIGURE 1D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31 DK11
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1 GTGGAAGTCAGGAACATCAGTTCTAGCTACTAtGCCACCAATGATTGCTCAAACAgCAGCA
1 GTGGAAGTCAGGAACAcCAGTTCTAGtTACTAcGCCACCAATGATTGCTCAAACAaCAGCA
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184 GCACTcACTCAcAACCTGCGAACgCAtGTCGACGTGATCGTAATGGCAGCTACGGTCTGCT
184 GCACTtACTCAtAACCTGCGAACACACGTCGACGTGATCGTAATGGCAGCTACGGTCTGCT
184 GCgCTCACTCACAACCTGCGAGCACACGTCGATATGATCGTAATGGCAGCTACGGTCTGCT
184 GCaCTCACTCACAACCTGCGAGCACAtaTaGATATGATtGTAATGGCAGCTACGGTCTGCT
GCaCTcACTCAcAACCTGCGA-CaCA-gTcGA--TGATcGTAATGGCAGCTACGGTCTGCT
245 CGGCCTTGTATGTGGGgGACGTgTGCGGGGCCGTGATGATaGcGTCGCAGGCTtTCATAAT
245 CGGCCTTGTATGTGGGAGACGTaTGCGGGGCCGTGATGATCGTGTCGCAGGCTcTCATAAT
245 CGGCCTTGTATGTGGGAGACaTGTGCGGGGCCGTGATGATCGTGTCGCAGGCTTTCATAAT
245 CGGCCTTGTATGTGGGAGACgTGTGCGGGGCCGTGATGATCGTGTCGCAGGCTTTCATAgT
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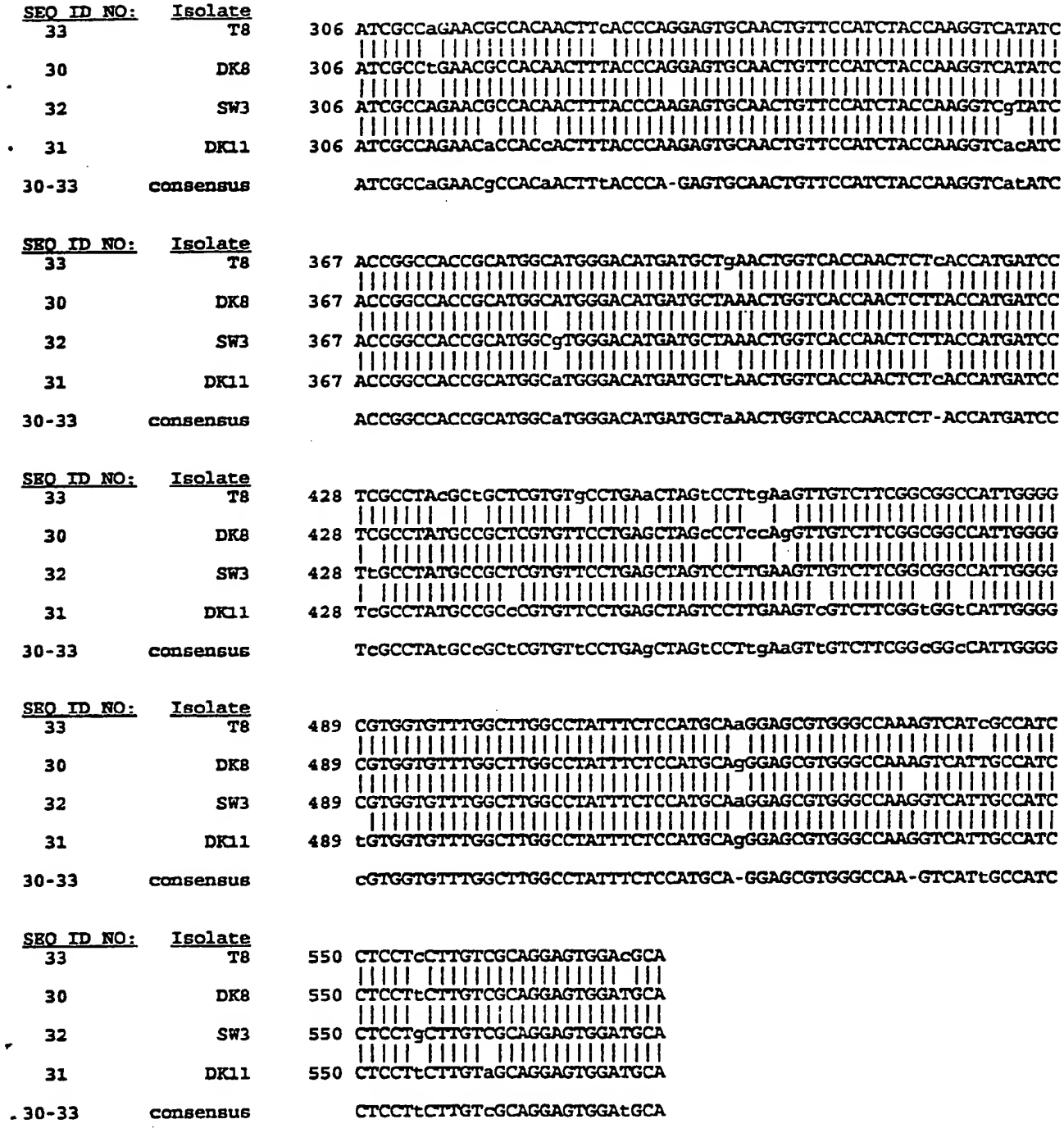
FIGURE 1D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30 DK8 306 ATCGCCtGAACGCCACAACTTTACCCAGGAGTGCAACTGTTCCATCTACCAAGGTCATATC
32 SW3 306 ATCGCCAGAACGCCACAACTTTACCCAAGAGTGCAACTGTTCCATCTACCAAGGTCgTATC
31 DK11 306 ATCGCCAGAACaCCACcACTTTACCCAAGAGTGCAACTGTTCCATCTACCAAGGTCacATC
30-33 consensus ATCGCCaGAACgCCACaACTTtACCCA-GAGTGCAACTGTTCCATCTACCAAGGTCatATC
SEQ ID NO: Isolate
33 T8 367 ACCGGCCACCGCATGGCATGGGACATGATGCTgAACTGGTCACCAACTCTcACCATGATCC
30 DK8 367 ACCGGCCACCGCATGGCATGGGACATGATGCTAAACTGGTCACCAACTCTTACCATGATCC
32 SW3 367 ACCGGCCACCGCATGGCgTGGGACATGATGCTAAACTGGTCACCAACTCTTACCATGATCC
31 DK11 367 ACCGGCCACCGCATGGCaTGGGACATGATGCTtAACTGGTCACCAACTCTcACCATGATCC
30-33 consensus ACCGGCCACCGCATGGCaTGGGACATGATGCTaAACTGGTCACCAACTCT-ACCATGATCC
SEQ ID NO: Isolate
33 T8 428 TCGCCTAcGCtGCTCGTGTgCCTGAaCTAGtCCTtgAaGTTGTCTTCGGCGGCCATTGGGG
30 DK8 428 TCGCCTATGCCGCTCGTGTTCCTGAGCTAGcCCTccAgGTTGTCTTCGGCGGCCATTGGGG
32 SW3 428 TtGCCTATGCCGCTCGTGTTCCTGAGCTAGTCCTTGAAGTTGTCTTCGGCGGCCATTGGGG
31 DK11 428 TcGCCTATGCCGCcCGTGTTCCTGAGCTAGTCCTTGAAGTcGTCTTCGGtGGtCATTGGGG
30-33 consensus TcGCCTAtGCcGCtCGTGTtCCTGAgCTAGtCCTtgAaGTtGTCTTCGGcGGcCATTGGGG
SEQ ID NO: Isolate
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30 DK8 489 CGTGGTGTTTGGCTTGGCCTATTTCTCCATGCAgGGAGCGTGGGCCAAAGTCATTGCCATC
32 SW3 489 CGTGGTGTTTGGCTTGGCCTATTTCTCCATGCAaGGAGCGTGGGCCAAGGTCATTGCCATC
31 DK11 489 tGTGGTGTTTGGCTTGGCCTATTTCTCCATGCAgGGAGCGTGGGCCAAGGTCATTGCCATC
30-33 consensus cGTGGTGTTTGGCTTGGCCTATTTCTCCATGCA-GGAGCGTGGGCCAA-GTCATtGCCATC
SEQ ID NO: Isolate
33 T8 550 CTCCTcCTTGTCGCAGGAGTGGAcGCA
30 DK8 550 CTCCTtCTTGTCGCAGGAGTGGATGCA
32 SW3 550 CTCCTgCTTGTCGCAGGAGTGGATGCA
31 DK11 550 CTCCTtCTTGTaGCAGGAGTGGATGCA
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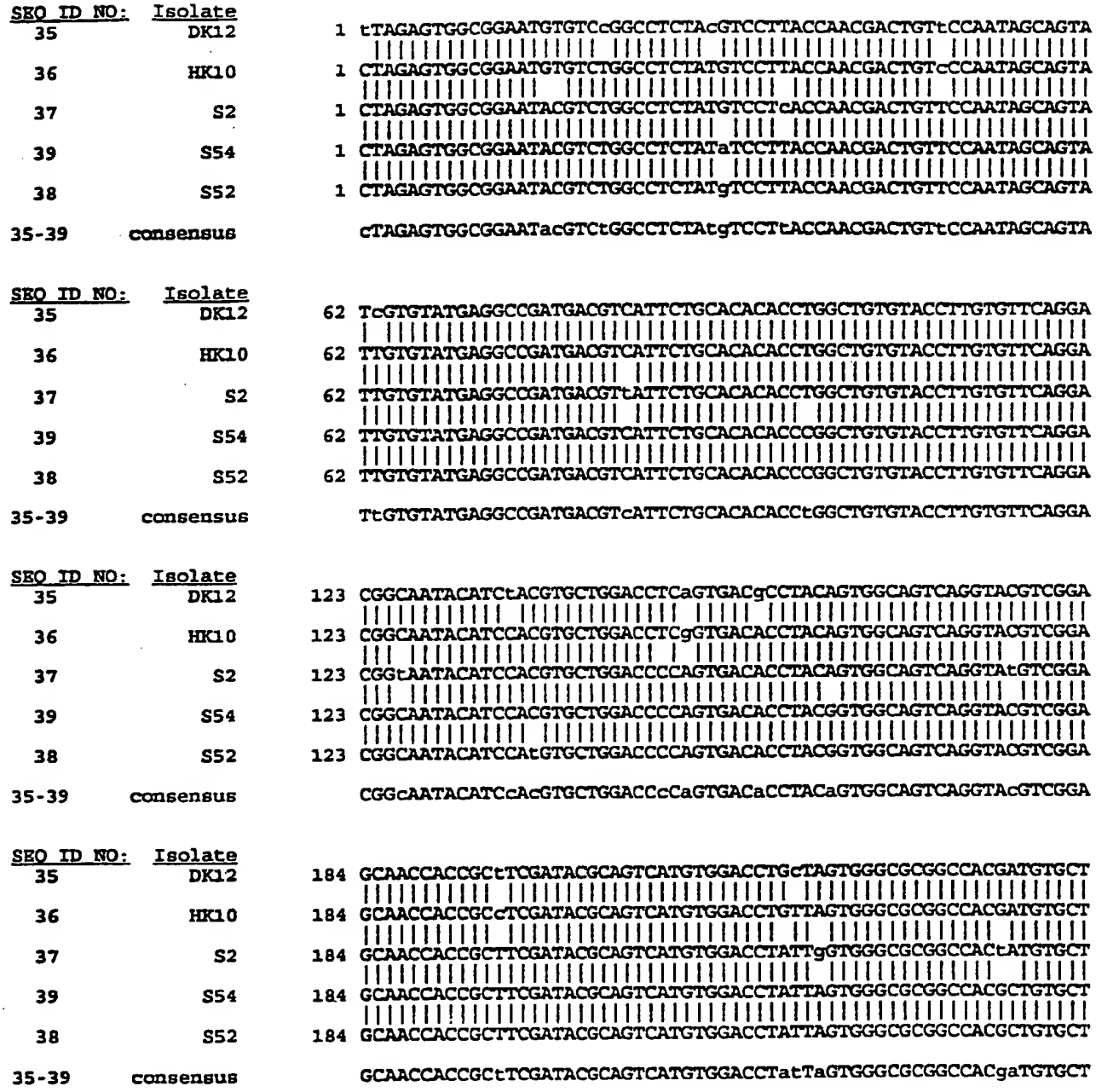
FIGURE 1E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36 HK10 1 CTAGAGTGGCGGAATGTGTCTGGCCTCTATGTCCTTACCAACGACTGTcCCAATAGCAGTA
37 S2 1 CTAGAGTGGCGGAATACGTCTGGCCTCTATGTCCTcACCAACGACTGTTCCAATAGCAGTA
39 S54 1 CTAGAGTGGCGGAATACGTCTGGCCTCTATaTCCTTACCAACGACTGTTCCAATAGCAGTA
38 S52 1 CTAGAGTGGCGGAATACGTCTGGCCTCTATgTCCTTACCAACGACTGTTCCAATAGCAGTA
35-39 consensus cTAGAGTGGCGGAATacGTCtGGCCTCTAtgTCCTtACCAACGACTGTtCCAATAGCAGTA
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37 S2 62 TTGTGTATGAGGCCGATGACGTtATTCTGCACACACCTGGCTGTGTACCTTGTGTTCAGGA
39 S54 62 TTGTGTATGAGGCCGATGACGTCATTCTGCACACACCCGGCTGTGTACCTTGTGTTCAGGA
38 S52 62 TTGTGTATGAGGCCGATGACGTCATTCTGCACACACCCGGCTGTGTACCTTGTGTTCAGGA
35-39 consensus TtGTGTATGAGGCCGATGACGTcATTCTGCACACACCtGGCTGTGTACCTTGTGTTCAGGA
SEQ ID NO: Isolate
35 DK12 123 CGGCAATACATCCtACGTGCTGGACCTCaGTGACgCCTACAGTGGCAGTCAGGTACGTCGGA
36 HK10 123 CGGCAATACATCCACGTGCTGGACCTCgGTGACACCTACAGTGGCAGTCAGGTACGTCGGA
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38 S52 123 CGGCAATACATCCAtGTGCTGGACCCCAGTGACACCTACGGTGGCAGTCAGGTACGTCGGA
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36 HK10 184 GCAACCACCGCcTCGATACGCAGTCATGTGGACCTGTTAGTGGGCGCGGCCACGATGTGCT
37 S2 184 GCAACCACCGCTTCGATACGCAGTCATGTGGACCTATTgGTGGGCGCGGCCACtATGTGCT
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38 S52 184 GCAACCACCGCTTCGATACGCAGTCATGTGGACCTATTAGTGGGCGCGGCCACGCTGTGCT
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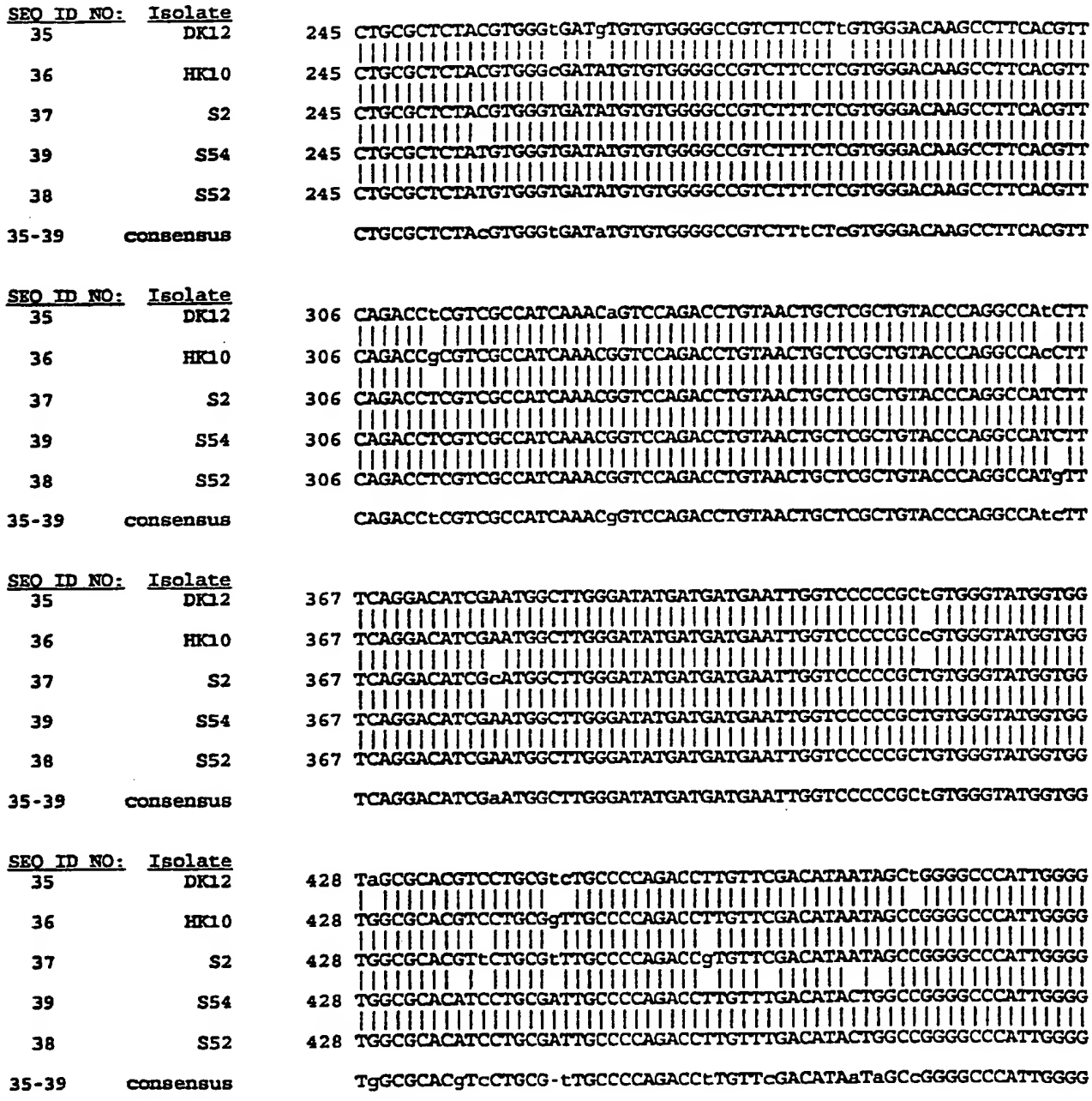
FIGURE 1E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39 S54 245 CTGCGCTCTATGTGGGTGATATGTGTGGGGCCGTCTTTCTCGTGGGACAAGCCTTCACGTT
38 S52 245 CTGCGCTCTATGTGGGTGATATGTGTGGGGCCGTCTTTCTCGTGGGACAAGCCTTCACGTT
35-39 consensus CTGCGCTCTAcGTGGGtGATaTGTGTGGGGCCGTCTTTcTCcGTGGGACAAGCCTTCACGTT
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36 HK10 306 CAGACCgCGTCGCCATCAAACGGTCCAGACCTGTAACTGCTCGCTGTACCCAGGCCAcCTT
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36 HK10 367 TCAGGACATCGAATGGCTTGGGATATGATGATGAATTGGTCCCCCGCcGTGGGTATGGTGG
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35-39 consensus TCAGGACATCGaATGGCTTGGGATATGATGATGAATTGGTCCCCCGCtGTGGGTATGGTGG
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39 S54 428 TGGCGCACATCCTGCGATTGCCCCAGACCTTGTTTGACATACTGGCCGGGGCCCATTGGGG
38 S52 428 TGGCGCACATCCTGCGATTGCCCCAGACCTTGTTTGACATACTGGCCGGGGCCCATTGGGG
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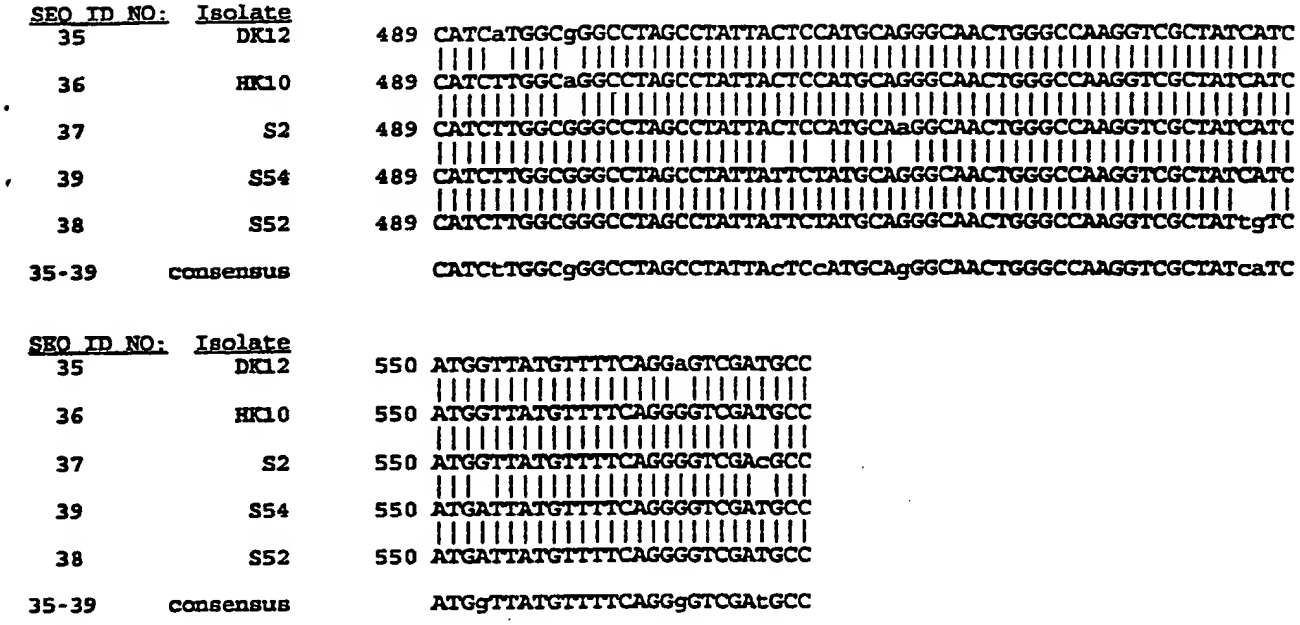
FIGURE 1E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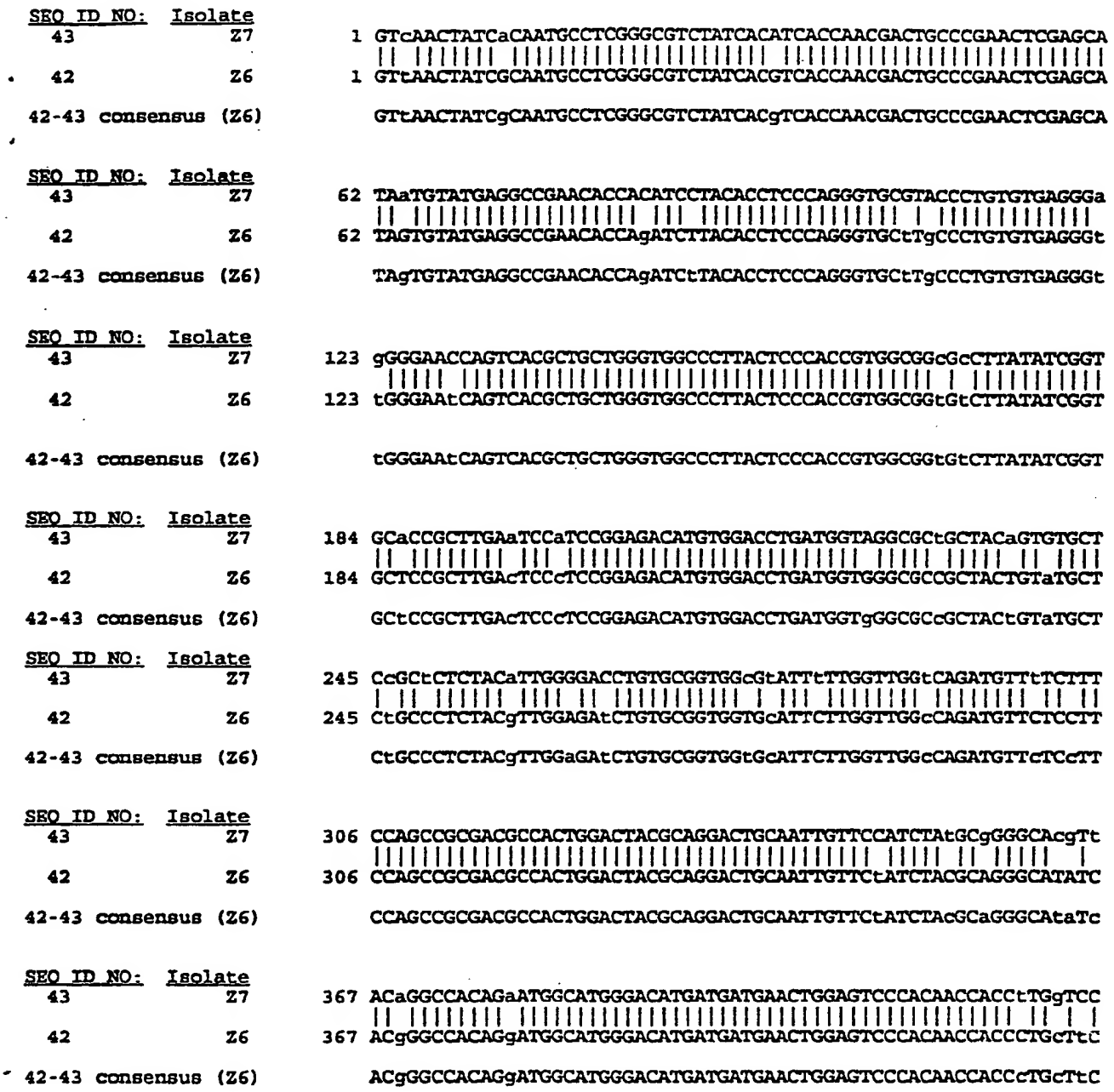
39 S54 489 CATCTTGGCGGGCCTAGCCTATTATTCTATGCAGGGCAACTGGGCCAAGGTCGCTATCATC
38 S52 489 CATCTTGGCGGGCCTAGCCTATTATTCTATGCAGGGCAACTGGGCCAAGGTCGCTATtgTC
35-39 consensus CATCtTGGCgGGCCTAGCCTATTAcTCcATGCAgGGCAACTGGGCCAAGGTCGCTATcaTC
SEQ ID NO: Isolate
35 DK12 550 ATGGTTATGTTTTCAGGaGTCGATGCC
36 HK10 550 ATGGTTATGTTTTCAGGGGTCGATGCC
37 S2 550 ATGGTTATGTTTTCAGGGGTCGAcGCC
39 S54 550 ATGATTATGTTTTCAGGGGTCGATGCC
38 S52 550 ATGATTATGTTTTCAGGGGTCGATGCC
35-39 consensus ATGgTTATGTTTTCAGGgGTCGAtGCC

FIGURE 1F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42 Z6 1 GTtAACTATCGCAATGCCTCGGGCGTCTATCACGTCACCAACGACTGCCCGAACTCGAGCA
42-43 consensus (Z6) GTtAACTATCgCAATGCCTCGGGCGTCTATCACgTCACCAACGACTGCCCGAACTCGAGCA
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43 Z7 62 TAaTGTATGAGGCCGAACACCACATCCTACACCTCCCAGGGTGCGTACCCTGTGTGAGGGa
42 Z6 62 TAGTGTATGAGGCCGAACACCAgATCTTACACCTCCCAGGGTGCtTgCCCTGTGTGAGGGt
42-43 consensus (Z6) TAgTGTATGAGGCCGAACACCAgATCtTACACCTCCCAGGGTGCtTgCCCTGTGTGAGGGt
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43 Z7 123 gGGGAACCAGTCACGCTGCTGGGTGGCCCTTACTCCCACCGTGGCGGcGcCTTATATCGGT
42 Z6 123 tGGGAAtCAGTCACGCTGCTGGGTGGCCCTTACTCCCACCGTGGCGGtGtCTTATATCGGT
42-43 consensus (Z6) tGGGAAtCAGTCACGCTGCTGGGTGGCCCTTACTCCCACCGTGGCGGtGtCTTATATCGGT
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42-43 consensus (Z6) GCtCCGCTTGAcTCCcTCCGGAGACATGTGGACCTGATGGTgGGCGCcGCTACtGTaTGCT
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42 Z6 245 CtGCCCTCTACgTTGGAGAtCTGTGCGGTGGTGcATTCTTGGTTGGcCAGATGTTCTCCTT
42-43 consensus (Z6) CtGCCCTCTACgTTGGaGAtCTGTGCGGTGGtGcATTCTTGGTTGGcCAGATGTTcTCcTT
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42 Z6 306 CCAGCCGCGACGCCACTGGACTACGCAGGACTGCAATTGTTCtATCTACGCAGGGCATATC
42-43 consensus (Z6) CCAGCCGCGACGCCACTGGACTACGCAGGACTGCAATTGTTCtATCTAcGCaGGGCAtaTc
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43 Z7 367 ACaGGCCACAGaATGGCATGGGACATGATGATGAACTGGAGTCCCACAACCACCtTGgTCC
42 Z6 367 ACgGGCCACAGgATGGCATGGGACATGATGATGAACTGGAGTCCCACAACCACCCTGcTtC
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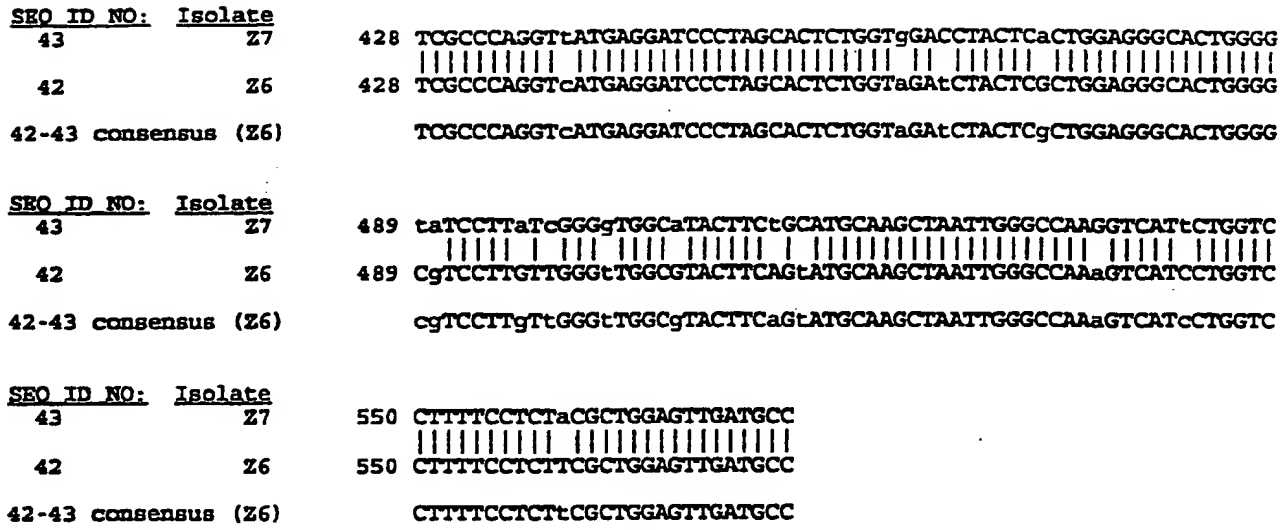
FIGURE 1F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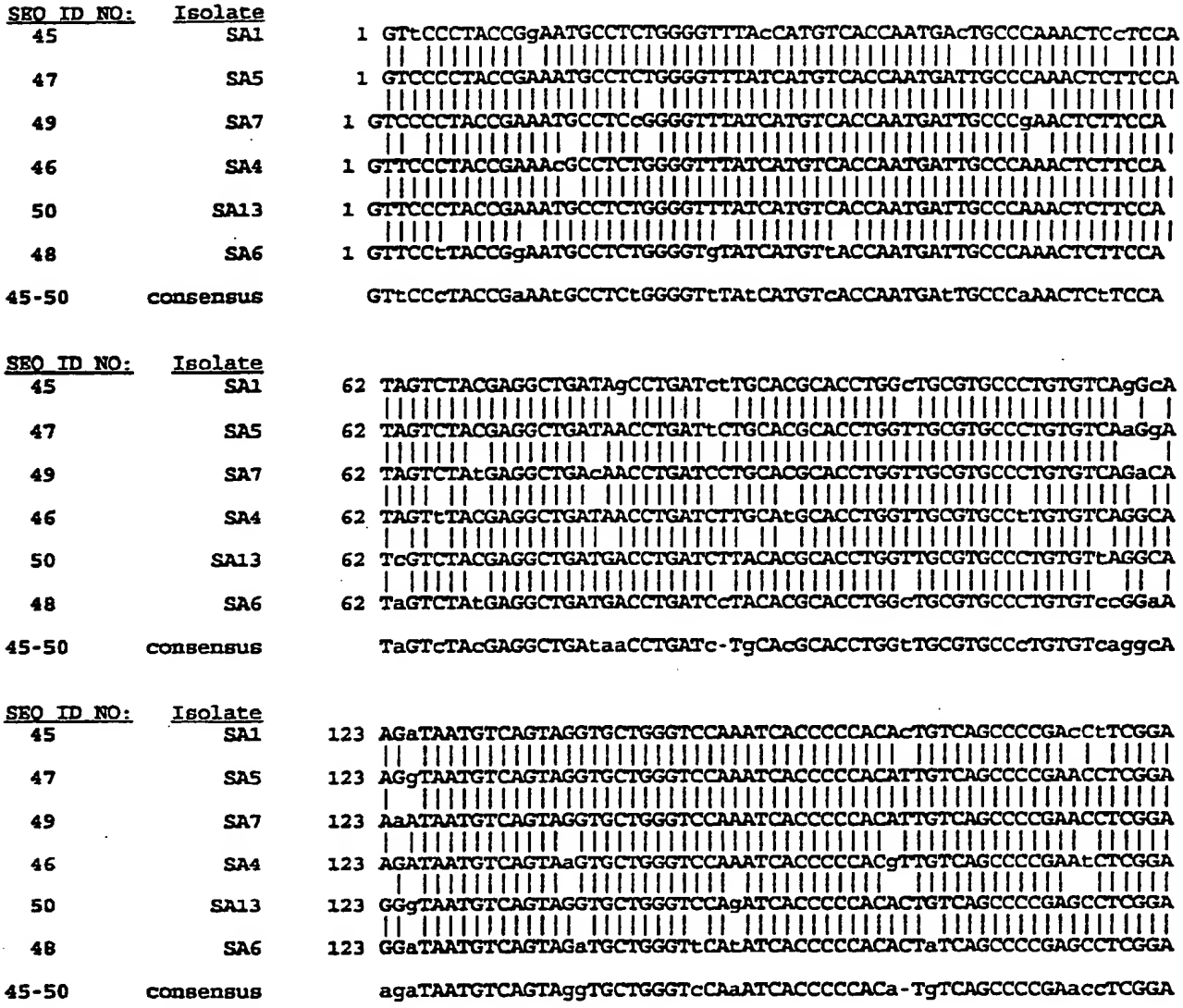
42 Z6 428 TCGCCCAGGTcATGAGGATCCCTAGCACTCTGGTaGAtCTACTCgCTGGAGGGCACTGGGG
42-43 consensus (Z6) TCGCCCAGGTcATGAGGATCCCTAGCACTCTGGTaGAtCTACTCgCTGGAGGGCACTGGGG
SEQ ID NO: Isolate
43 Z7 489 taTCCTTaTcGGGgTGGCaTACTTCtGCATGCAAGCTAATTGGGCCAAGGTCATtCTGGTC
42 Z6 489 CgTCCTTgTTGGGtTGGCgTACTTCAGtATGCAAGCTAATTGGGCCAAaGTCATCCTGGTC
42-43 consensus (Z6) cgTCCTTgTtGGGtTGGCgTACTTCaGtATGCAAGCTAATTGGGCCAAaGTCATcCTGGTC
SEQ ID NO: Isolate
43 Z7 550 CTTTTCCTCTaCGCTGGAGTTGATGCC
42 Z6 550 CTTTTCCTCTTCGCTGGAGTTGATGCC
42-43 consensus (Z6) CTTTTCCTCTtCGCTGGAGTTGATGCC

FIGURE 1G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49 SA7 1 GTCCCCTACCGAAATGCCTCcGGGGTTTATCATGTCACCAATGATTGCCCgAACTCTTCCA
46 SA4 1 GTTCCCTACCGAAAcGCCTCTGGGGTTTATCATGTCACCAATGATTGCCCAAACTCTTCCA
50 SA13 1 GTTCCCTACCGAAATGCCTCTGGGGTTTATCATGTCACCAATGATTGCCCAAACTCTTCCA
48 SA6 1 GTTCCtTACCGgAATGCCTCTGGGGTgTATCATGTtACCAATGATTGCCCAAACTCTTCCA
45-50 consensus GTtCCcTACCGaAAtGCCTCtGGGGTtTAtCATGTcACCAATGAtTGCCCaAACTCtTCCA
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47 SA5 62 TAGTCTACGAGGCTGATAACCTGATtCTGCACGCACCTGGTTGCGTGCCCTGTGTCAaGgA
49 SA7 62 TAGTCTAtGAGGCTGAcAACCTGATCCTGCACGCACCTGGTTGCGTGCCCTGTGTCAGaCA
46 SA4 62 TAGTtTACGAGGCTGATAACCTGATCTTGCAtGCACCTGGTTGCGTGCCtTGTGTCAGGCA
50 SA13 62 TcGTCTACGAGGCTGATGACCTGATCTTACACGCACCTGGTTGCGTGCCCTGTGTtAGGCA
48 SA6 62 TaGTCTAtGAGGCTGATGACCTGATCcTACACGCACCTGGcTGCGTGCCCTGTGTccGGaA
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47 SA5 123 AGgTAATGTCAGTAGGTGCTGGGTCCAAATCACCCCCACATTGTCAGCCCCGAACCTCGGA
49 SA7 123 AaATAATGTCAGTAGGTGCTGGGTCCAAATCACCCCCACATTGTCAGCCCCGAACCTCGGA
46 SA4 123 AGATAATGTCAGTAaGTGCTGGGTCCAAATCACCCCCACgTTGTCAGCCCCGAAtCTCGGA
50 SA13 123 GGgTAATGTCAGTAGGTGCTGGGTCCAgATCACCCCCACACTGTCAGCCCCGAGCCTCGGA
48 SA6 123 GGaTAATGTCAGTAGaTGCTGGGTtCAtATCACCCCCACACTaTCAGCCCCGAGCCTCGGA
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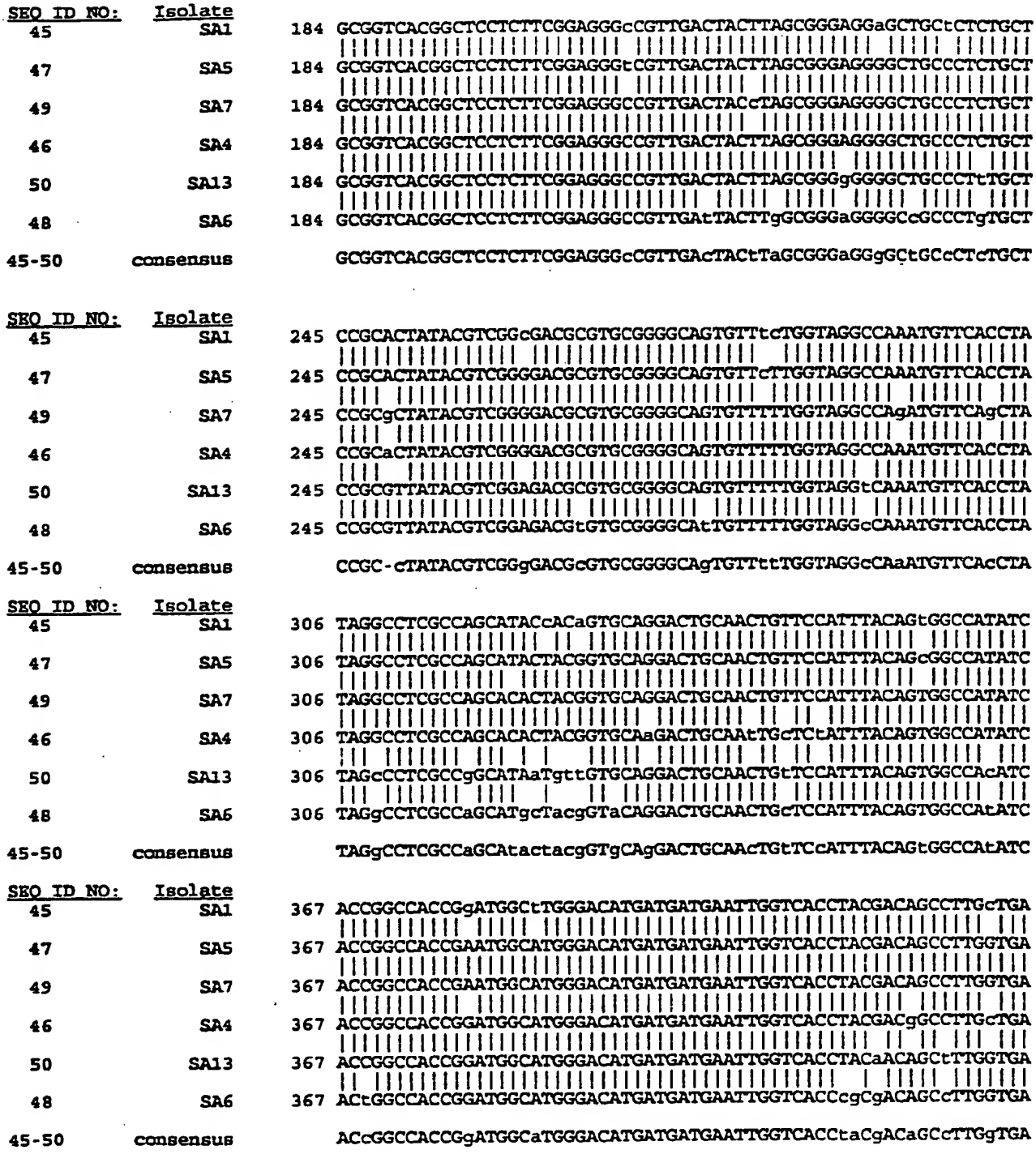
FIGURE 1G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49 SA7 184 GCGGTCACGGCTCCTCTTCGGAGGGCCGTTGACTACcTAGCGGGAGGGGCTGCCCTCTGCT
46 SA4 184 GCGGTCACGGCTCCTCTTCGGAGGGCCGTTGACTACTTAGCGGGAGGGGCTGCCCTCTGCT
50 SA13 184 GCGGTCACGGCTCCTCTTCGGAGGGCCGTTGACTACTTAGCGGGgGGGGCTGCCCTtTGCT
48 SA6 184 GCGGTCACGGCTCCTCTTCGGAGGGCCGTTGAtTACTTgGCGGGaGGGGCcGCCCTgTGCT
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49 SA7 245 CCGCgCTATACGTCGGGGACGCGTGCGGGGCAGTGTTTTTGGTAGGCCAgATGTTCAgCTA
46 SA4 245 CCGCaCTATACGTCGGGGACGCGTGCGGGGCAGTGTTTTTGGTAGGCCAAATGTTCACCTA
50 SA13 245 CCGCGTTATACGTCGGAGACGCGTGCGGGGCAGTGTTTTTGGTAGGtCAAATGTTCACCTA
48 SA6 245 CCGCGTTATACGTCGGAGACGtGTGCGGGGCAtTGTTTTTGGTAGGcCAAATGTTCACCTA
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46 SA4 306 TAGGCCTCGCCAGCACACTACGGTGCAaGACTGCAAtTGcTCtATTTACAGTGGCCATATC
50 SA13 306 TAGcCCTCGCCgGCATAaTgttGTGCAGGACTGCAACTGtTCCATTTACAGTGGCCAcATC
48 SA6 306 TAGgCCTCGCCaGCATgcTacgGTaCAGGACTGCAACTGcTCCATTTACAGTGGCCAtATC
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49 SA7 367 ACCGGCCACCGAATGGCATGGGACATGATGATGATGAATTGGTCACCTACGACAGCCTTGGTGA
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50 SA13 367 ACCGGCCACCGGATGGCATGGGACATGATGATGATGAATTGGTCACCTACaACAGCcTTGGTGA
48 SA6 367 ACtGGCCACCGGATGGCATGGGACATGATGATGATGAATTGGTCACCcgCgACAGCcTTGGTGA
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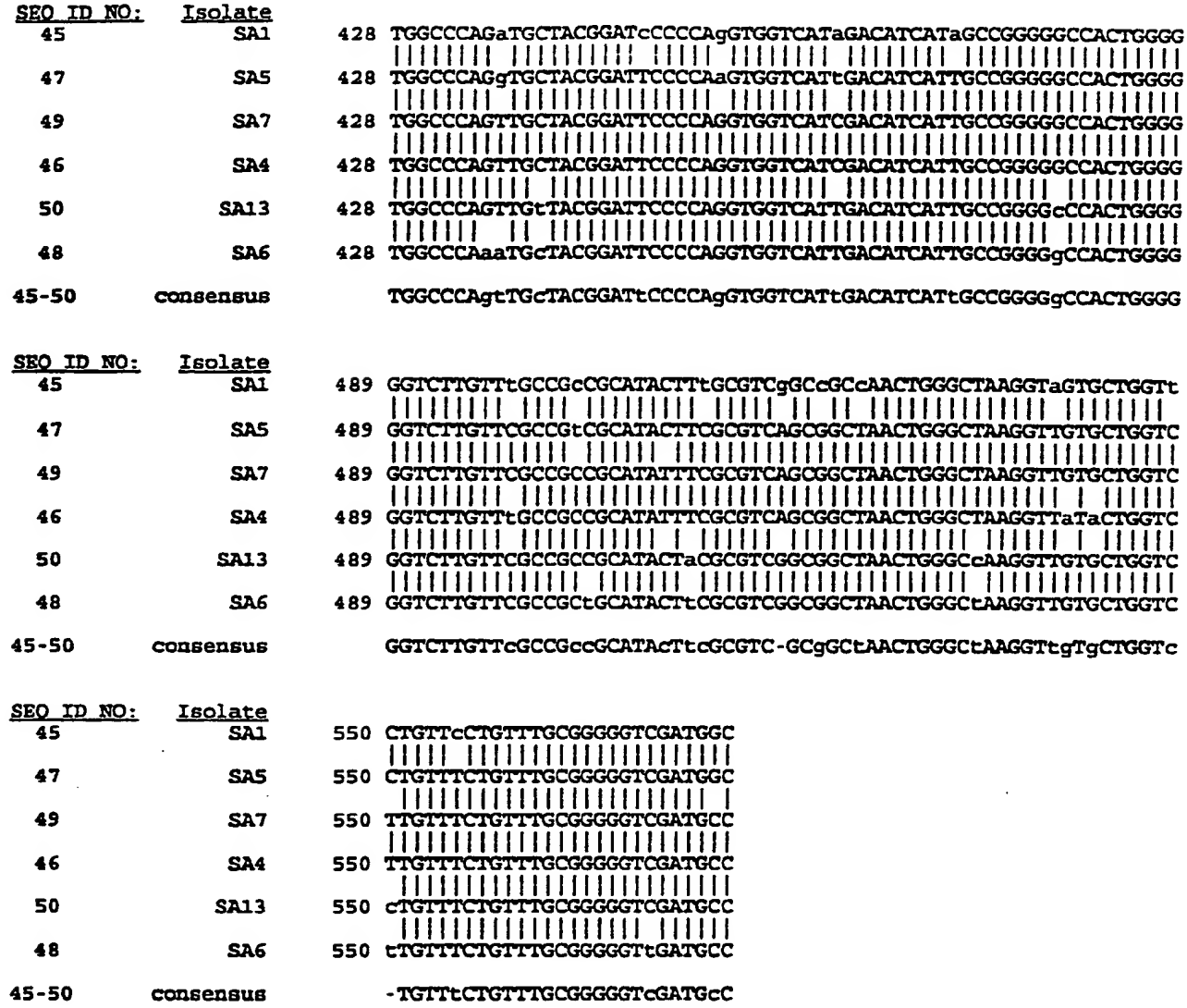
FIGURE 1G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49 SA7 428 TGGCCCAGTTGCTACGGATTCCCCAGGTGGTCATCGACATCATTGCCGGGGGCCACTGGGG
46 SA4 428 TGGCCCAGTTGCTACGGATTCCCCAGGTGGTCATCGACATCATTGCCGGGGGCCACTGGGG
50 SA13 428 TGGCCCAGTTGtTACGGATTCCCCAGGTGGTCATTGACATCATTGCCGGGGcCCACTGGGG
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48 SA6 489 GGTCTTGTTCGCCGCtGCATACTtCGCGTCGGCGGCTAACTGGGCtAAGGTTGTGCTGGTC
45-50 consensus GGTCTTGTTcGCCGccGCATAcTtcGCGTC-GCgGCtAACTGGGCtAAGGTTgTgCTGGTc
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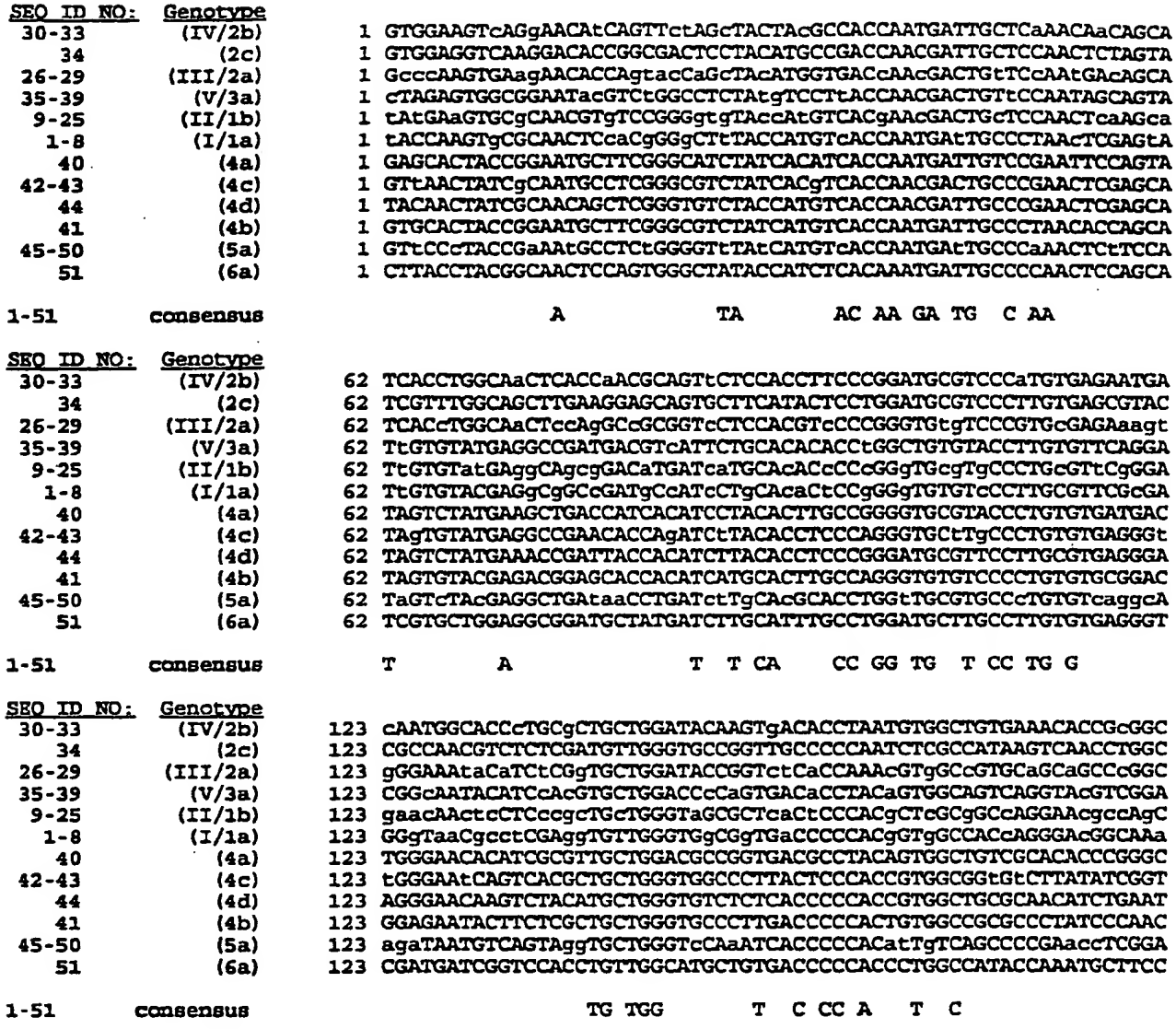
47 SA5 550 CTGTTTCTGTTTGCGGGGGTCGATGGC
49 SA7 550 TTGTTTCTGTTTGCGGGGGTCGATGCC
46 SA4 550 TTGTTTCTGTTTGCGGGGGTCGATGCC
50 SA13 550 cTGTTTCTGTTTGCGGGGGTCGATGCC
48 SA6 550 tTGTTTCTGTTTGCGGGGGTtGATGCC
45-50 consensus -TGTTtCTGTTTGCGGGGGTcGATGcC

FIGURE 1H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30-33 (IV/2b) 1 GTGGAAGTcAGgAACAtCAGTTctAGcTACTAcGCCACCAATGATTGCTCaAACAaCAGCA
34 (2c) 1 GTGGAGGTCAAGGACACCGGCGACTCCTACATGCCGACCAACGATTGCTCCAACTCTAGTA
26-29 (III/2a) 1 GcccAAGTGAagAACACCAgtacCaGcTAcATGGTGACcAAcGACTGtTCcAAtGAcAGCA
35-39 (V/3a) 1 cTAGAGTGGCGGAATacGTCtGGCCTCTAtgTCCTtACCAACGACTGTtCCAATAGCAGTA
9-25 (II/1b) 1 tAtGAaGTGCgCAACGTgTCCGGGgtgTAccAtGTCACgAAcGACTGcTCCAACTcaAGca
1-8 (I/1a) 1 tACCAAGTgCGCAACTCcaCgGGgCTtTACCATGTcACCAATGAtTGCCCTAAcTCGAGtA
40 (4a) 1 GAGCACTACCGGAATGCTTCGGGCATCTATCACATCACCAATGATTGTCCGAATTCCAGTA
42-43 (4c) 1 GTtAACTATCgCAATGCCTCGGGCGTCTATCACgTCACCAACGACTGCCCGAACTCGAGCA
44 (4d) 1 TACAACTATCGCAACAGCTCGGGTGTCTACCATGTCACCAACGATTGCCCGAACTCGAGCA
41 (4b) 1 GTGCACTACCGGAATGCTTCGGGCGTCTATCATGTCACCAATGATTGCCCTAACACCAGCA
45-50 (5a) 1 GTtCCcTACCGaAAtGCCTCtGGGGTtTAtCATGTcACCAATGAtTGCCCaAACTCtTCCA
51 (6a) 1 CTTACCTACGGCAACTCCAGTGGGCTATACCATCTCACAAATGATTGCCCCAACTCCAGCA
1-51 consensus A TA AC AA GA TG C AA
SEQ ID NO: Genotype
30-33 (IV/2b) 62 TCACCTGGCAaCTCACCaACGCAGTtCTCCACCTTCCCGGATGCGTCCCaTGTGAGAATGA
34 (2c) 62 TCGTTTGGCAGCTTGAAGGAGCAGTGCTTCATACTCCTGGATGCGTCCCTTGTGAGCGTAC
26-29 (III/2a) 62 TCACcTGGCAaCTccAgGCcGCGGTcCTCCACGTcCCCGGGTGtgTCCCGTGcGAGAaagt
35-39 (V/3a) 62 TtGTGTATGAGGCCGATGACGTcATTCTGCACACACCtGGCTGTGTACCTTGTGTTCAGGA
9-25 (II/1b) 62 TtGTGTatGAggCAgcgGACaTGATcaTGCAcACcCCcGGgTGcgTgCCCTGcGTtCgGGA
1-8 (I/1a) 62 TtGTGTACGAGgCgGCcGATgCcATcCTgCAcaCtCCgGGgTGTGTcCCTTGCGTTCGcGA
40 (4a) 62 TAGTCTATGAAGCTGACCATCACATCCTACACTTGCCGGGGTGCGTACCCTGTGTGATGAC
42-43 (4c) 62 TAgTGTATGAGGCCGAACACCAgATCtTACACCTCCCAGGGTGCtTgCCCTGTGTGAGGGt
44 (4d) 62 TAGTCTATGAAACCGATTACCACATCTTACACCTCCCGGGATGCGTTCCTTGCGTGAGGGA
41 (4b) 62 TAGTGTACGAGACGGAGCACCACATCATGCACTTGCCAGGGTGTGTCCCCTGTGTGCGGAC
45-50 (5a) 62 TaGTcTAcGAGGCTGAtaaCCTGATctTgCAcGCACCTGGtTGCGTGCCcTGTGTcaggcA
51 (6a) 62 TCGTGCTGGAGGCGGATGCTATGATCTTGCATTTGCCTGGATGCTTGCCTTGTGTGAGGGT
1-51 consensus T A T T CA CC GG TG T CC TG G
SEQ ID NO: Genotype
30-33 (IV/2b) 123 cAATGGCACCcTGCgCTGCTGGATACAAGTgACACCTAATGTGGCTGTGAAACACCGcGGC
34 (2c) 123 CGCCAACGTCTCTCGATGTTGGGTGCCGGTTGCCCCCAATCTCGCCATAAGTCAACCTGGC
26-29 (III/2a) 123 gGGAAAtaCaTCtCGgTGCTGGATACCGGTctCaCCAAAcGTgGCcGTGCaGCaGCCcGGC
35-39 (V/3a) 123 CGGcAATACATCCcAcGTGCTGGACCcCaGTGACaCCTACaGTGGCAGTCAGGTAcGTCGGA
9-25 (II/1b) 123 gaacAActcCTCccgcTGcTGGGTaGCGCTcaCtCCCACgCTcGCgGCcAGGAAcgccAgC
1-8 (I/1a) 123 GGgTaaCgcctCGAggTGTTGGGTGgCGgTGaCCCCCACgGTgGCCACcAGGGAcGGCAAa
40 (4a) 123 TGGGAACACATCGCGTTGCTGGACGCCGGTGACGCCTACAGTGGCTGTCGCACACCCGGGC
42-43 (4c) 123 tGGGAAtCAGTCACGCTGCTGGGTGGCCCTTACTCCCACCGTGGCGGtGtCTTATATCGGT
44 (4d) 123 AGGGAACAAGTCTACATGCTGGGTGTCTCTCACCCCCACCGTGGCTGCGCAACATCTGAAT
41 (4b) 123 GGAGAATACTTCTCGCTGCTGGGTGCCCTTGACCCCCACTGTGGCCGCGCCCTATCCCAAC
45-50 (5a) 123 agaTAATGTCAGTAggTGCTGGGTcCAaATCACCCCCACatTgTCAGCCCCGAaccTCGGA
51 (6a) 123 CGATGATCGGTCCACCTGTTGGCATGCTGTGACCCCCACCCTGGCCATACCAAATGCTTCC
1-51 consensus TG TGG T C CC A T C

FIGURE 1H

SEQ ID NO:	Genotype		
30-33	(IV/2b)	184	GCaCTcACTCAcAACCTGCGAaCaCAtgTcGAcaTGATcGTAATGGCAGCTACGGTCTGCT
34	(2c)	184	GCTCTCACTAAGGGCCTGCGAGCACACATCGATATCATCGTGATGTCTGCTACGGTCTGTT
26-29	(III/2a)	184	GCcCTcACGCAGGGCTTGCGGACgCACATcGACATGGTtGTGATGTCCGCCACGCTCTGCT
35-39	(V/3a)	184	GCAACCACCGCttCGATACGCAGTCATGTGGACCTatTaGTGGGCGCGGCCACgaTGTGCT
9-25	(II/1b)	184	gTCcCcACtAcGaCaATACGACgcCAcGTCGAtTTGCTCGTTGGGGCGGCTgctTTCTGcT
1-8	(I/1a)	184	CTCCCcgCAaCGCAgCTtCGACGTcACATCGAtCTGCTtGTcGGgAGcGCCACCCTCTGcT
40	(4a)	184	GCTCCGCTTGAGTCGTTCCGGCGACATGTGGACTTAATGGTAGGCGCGGCCACTTTGTGTT
42-43	(4c)	184	GCtCCGCTTGAcTCCcTCCGGAGACATGTGGACCTGATGGTgGGCGCcGCTACtGTaTGCT
44	(4d)	184	GCTCCGCTTGAGTCTTTGAGACGTCACGTGGATCTGATGGTGGGCGGCGCCACTCTCTGCT
41	(4b)	184	GCACCGTTAGAGTCCATGCGCAGGCATGTAGACCTGATGGTGGGTGCGGCTACTATGTGTT
45-50	(5a)	184	GCGGTCACGGCTCCTCTTCGGAGGGcCGTTGACTACtTaGCGGGaGGgGCtGCcCTcTGCT
51	(6a)	184	ACGCCCGCAACGGGATTCCGCAGGCATGTGGATCTTCTTGCGGGCGCCGCAGTGGTTTGCT
1-51	consensus		T G T GA T G GC T TG T

SEQ ID NO:	Genotype		
30-33	(IV/2b)	245	CGGCCTTGTATGTGGGaGACgTgTGCGGGGCCGTGATGATcGtGTCGCAGGCTtTCATAaT
34	(2c)	245	CTGCCCTTTATGTGGGGGACGTGTGTGGCGCGCTGATGCTGGCCGCTCAGGTCGTCGTCGT
26-29	(III/2a)	245	CcGCtCTtTACGTGGGGGAccTCTGCGGcGGGgTgATGCTCGCaGCcCAgATGTTCATTgT
35-39	(V/3a)	245	CTGCGCTCTAcGTGGGtGATaTGTGTGGGGCCGTCTTtCTcGTGGGACAAGCCTTCACGTT
9-25	(II/1b)	245	CCGctATGTAcGTGGGgGAtCTcTGCGGaTCtGTttTCCTcgTcTCcCAGcTGTTCACctT
1-8	(I/1a)	245	CGGCCCTCTAcGTGGGGGACtTGTGCGGGTCTGTCTTtCTtGTCgGtCAaCTGTTcACctT
40	(4a)	245	CTGCCCTCTATGTTGGGGACCTCTGCGGAGGTGCCTTCCTGATGGGGCAGATGATCACTTT
42-43	(4c)	245	CtGCCCTCTACgTTGGaGAtCTGTGCGGTGGtGcATTCTTGGTTGGcCAGATGTTcTCcTT
44	(4d)	245	CCGCCCTCTACATCGGAGACGTGTGTGGGGGTGTGTTCTTGGTCGGTCAACTGTTCACCTT
41	(4b)	245	CCGCCTTCTACATTGGAGATCTGTGTGGAGGCGTCTTCCTAGTGGGCCAGCTGTTCGACTT
45-50	(5a)	245	CCGCgcTATACGTCGGgGACGcGTGCGGGGCAgTGTTttTGGTAGGcCAaATGTTCAcCTA
51	(6a)	245	CATCCCTGTACATCGGGGACCTGTGTGGCTCTCTCTTTTTGGCGGGACAACTATTCACCTT
1-51	consensus		C T TA T GG GA TG GG T T CA T

SEQ ID NO:	Genotype		
30-33	(IV/2b)	306	ATCGCCaGAACgCCACaACTTtACCCAaGAGTGCAACTGTTCCATCTACCAAGGTCatATC
34	(2c)	306	GTCGCCACAACACCATACGTTTGTCCAGGAATGCAACTGTTCCATATACCCGGGCCGCATT
26-29	(III/2a)	306	CTCGCCGCaaCacCACTgGTTTGTGCAaGAaTGCAAtTGCTCcATcTACCCtGGtACCATC
35-39	(V/3a)	306	CAGACCtCGTCGCCATCAAACgGTCCAGACCTGTAACTGCTCGCTGTACCCAGGCCAtcTT
9-25	(II/1b)	306	cTCgCCtCGcCggcAtgaGACagtaCAGgAcTGcAAcTGcTCaaTCTATCCcGGcCacgTa
1-8	(I/1a)	306	cTCtCCCAGgCgCCaCTGGACaACGCAaGaCTGcAAtTGTTCtATCTAtCCcGGCCAtATa
40	(4a)	306	TCGGCCGCGTCGCCACTGGACCACGCAGGAGTGCAATTGTTCCATCTACACTGGCCATATC
42-43	(4c)	306	CCAGCCGCGACGCCACTGGACTACGCAGGACTGCAATTGTTCtATCTAcGCaGGGCAtaTc
44	(4d)	306	CCAACCTCGCCGCCACTGGACCACCCAAGACTGCAATTGTTCCATCTACACAGGACATATC
41	(4b)	306	CCGACCGCGCCGGCACTGGACCACCCAGGATTGCAACTGCTCCATCTATCCTGGTCACGTC
45-50	(5a)	306	TAGgCCTCGCCaGCAtactacgGTgCAgGACTGCAAcTGtTCcATTTACAGtGGCCAtATC
51	(6a)	306	TCAGCCCCGCCGTCATTGGACTGTGCAAGACTGCAACTGCTCCATCTATACAGGCCACGTC
1-51	consensus		CC C CA TG AA TG TC T TA GG T

SEQ ID NO:	Genotype		
30-33	(IV/2b)	367	ACCGGCCACCGCATGGCaTGGGACATGATGCTaAACTGGTCACCAACTCTtACCATGATCC
34	(2c)	367	ACGGGACACCGCATGGCTTGGGATATGATGATGAACTGGTCGCCCACTACCACCATGCTCC
26-29	(III/2a)	367	ACtGGaCACCGTATGGCATGGGAcATGATGATGAACTGGTCGCCCACggCCACcaTGATCc
35-39	(V/3a)	367	TCAGGACATCGaATGGCTTGGGATATGATGATGAATTGGTCCCCCGCtGTGGGTATGGTGG
9-25	(II/1b)	367	tCAGGTCAcCGcATGGCtTGGGAtATGATGATGAAcTGGTCaCCtACAgCaGCccTaGTgg
1-8	(I/1a)	367	ACGGGtCAcCGcATGGCaTGGGATATGATGATGAACTGGTCCCCtACgaCgGCgcTGGTag
40	(4a)	367	ACCGGCCACAGGATGGCGTGGGACATGATGATGAACTGGAGCCCTACCACCACTCTGCTCC
42-43	(4c)	367	ACgGGCCACAGgATGGCATGGGACATGATGATGAACTGGAGTCCCACAACCACCcTGcTtC
44	(4d)	367	ACAGGACACAGAATGGCTTGGGACATGATGATGAATTGGAGCCCCACTGCGACGCTGGTCC
41	(4b)	367	TCGGGCCACAGGATGGCCTGGGACATGATGATGAACTGGAGCCCTACCAGCGCGCTGATTA
45-50	(5a)	367	ACcGGCCACCGgATGGCaTGGGACATGATGATGAATTGGTCACCtaCgACaGCcTTGgTGA
51	(6a)	367	ACCGGCCACAGGATGGCTTGGGACATGATGATGAACTGGTCACCCACAACCACTCTGGTCC
1-51	consensus		C GG CA G ATGGC TGGGA ATGATG T AA TGG CC C T T

FIGURE 1H

SEQ ID NO:	Genotype		
30-33	(IV/2b)	428	TcGCCTAtGCcGCtCGTGTtCCTGAgCTAGtCCTtgAaGTtGTCTTCGGcGGcCATTGGGG
34	(2c)	428	TGGCGTACTTGGTGCGCATCCCGGAAGTCATCTTGGATATTGTTACAGGAGGTCATTGGGG
26-29	(III/2a)	428	TGGCGTACGcGATGCGCGTTCCCGAGGTCATCaTAGACATCaTtaGCGGgGCtCAcTGGGG
35-39	(V/3a)	428	TgGCGCACgTcCTGCGttTGCCCCAGACCtTGTTcGACATAaTaGCcGGGGCCCATTGGGG
9-25	(II/1b)	428	TaTCGCAgtTaCTCCGgaTCCCaCAAGCTgTCgTGGAcaTGGTggCgGGgGCCCACTGGGG
1-8	(I/1a)	428	TaGCtCAGCTGCTCcGGaTCCCgCAaGCCaTCTTGGAcATGATCGCTGGtGCcCACTGGGG
40	(4a)	428	TCGCCCAGATCATGAGGGTCCCCACAGCCTTTCTCGACATGGTTGCCGGAGGCCACTGGGG
42-43	(4c)	428	TCGCCCAGGTcATGAGGATCCCTAGCACTCTGGTaGAtCTACTCgCTGGAGGGCACTGGGG
44	(4d)	428	TCGCCCAACTTATGAGGATCCCAGGCGCCATGGTCGACCTGCTTGCAGGCGGCCACTGGGG
41	(4b)	428	TGGCTCAGATCTTACGGATCCCCTCTATCCTAGGTGACTTGCTCACCGGGGGTCACTGGGG
45-50	(5a)	428	TGGCCCAgtTGcTACGGATtCCCCAgGTGGTCATtGACATCATtGCCGGGGgCCACTGGGG
51	(6a)	428	TATCTAGCATCTTGAGGGTACCTGAGATTTGTGCGAGTGTGATATTTGGTGGCCATTGGGG
1-51	consensus		T C G T CC T T GG G CA TGGGG

SEQ ID NO:	Genotype		
30-33	(IV/2b)	489	cGTGGTGTTTGGCTTGGCCTATTTCTCCATGCAgGGAGCGTGGGCCAAaGTCATtGCCATC
34	(2c)	489	TGTAATGTTTGGCCTCGCTTACTTCTCCATGCAGGGATCGTGGGCGAAGGTCATCGTTATC
26-29	(III/2a)	489	CGTCaTGTTcGGCtTaGCCTACTTCTCTATGCAGGGAGCGTGGGCGAAaGTCgTTGTCATC
35-39	(V/3a)	489	CATCtTGGCgGGCCTAGCCTATTAcTCcATGCAgGGCAACTGGGCCAAGGTCGCTATcaTC
9-25	(II/1b)	489	agTCCTgGCGGGCCTtGCcTACTAtTCCATGGtgGGgAACTGGGCtAAGGTttTgATTGTg
1-8	(I/1a)	489	AGTCCTaGCGGGCATAGCGTATTTcTCCATGGtGGGgAACTGGGCGAAGGTCcTggTaGTg
40	(4a)	489	CGTCCTCGCGGGCTTGGCGTACTTCAGCATGCAAGGCAATTGGGCCAAGGTAGTCCTGGTC
42-43	(4c)	489	cgTCCTTgTtGGGtTGGCgTACTTCaGtATGCAAGCTAATTGGGCCAAaGTCATcCTGGTC
44	(4d)	489	CATTCTGGTTGGCATAGCGTACTTCAGCATGCAAGCTAATTGGGCCAAGGTTATCCTGGTC
41	(4b)	489	AGTTCTTGCTGGTCTAGCTTTCTTCAGCATGCAGAGTAACTGGGCGAAGGTCATCCTGGTC
45-50	(5a)	489	GGTCTTGTTcGCCGccGCATAcTtcGCGTCgGCgGCtAACTGGGCtAAGGTtgTgCTGGTc
51	(6a)	489	GATACTACTAGCCGTTGCCTACTTTGGCATGGCTGGCAACTGGCTAAAAGTTCTGGCTGTT
1-51	consensus		T T G GC T T TGG AA GT T

SEQ ID NO:	Genotype		
30-33	(IV/2b)	550	CTCCTtCTTGTcGCAGGAGTGGAtGCA
34	(2c)	550	CTCCTGCTGACTGCTGGGGTGGAGGCG
26-29	(III/2a)	550	CTttTGCTggCcGCTGGgGTGGACGCG
35-39	(V/3a)	550	ATGgTTATGTTTTCAGGgGTCGAtGCC
9-25	(II/1b)	550	aTGCTACTcTTTGCcGGcGTtGAcGGg
1-8	(I/1a)	550	CTGtTGCTgTTtgCCGGCGTcGAtGCG
40	(4a)	550	CTTTTCCTCTTTGCTGGGGTAGACGCC
42-43	(4c)	550	CTTTTCCTCTtCGCTGGAGTTGATGCC
44	(4d)	550	CTGTTTCTCTTTGCTGGAGTCGACGCT
41	(4b)	550	CTATTCCTCTTTGCCGGGGTCGAGGGA
45-50	(5a)	550	tTGTTtCTGTTTGCGGGGGTcGATGcC
51	(6a)	550	CTGTTCCTATTTGCAGGGGTTGAAGCA
1-51	consensus		T T T C GG GT GA G

FIGURE 2A

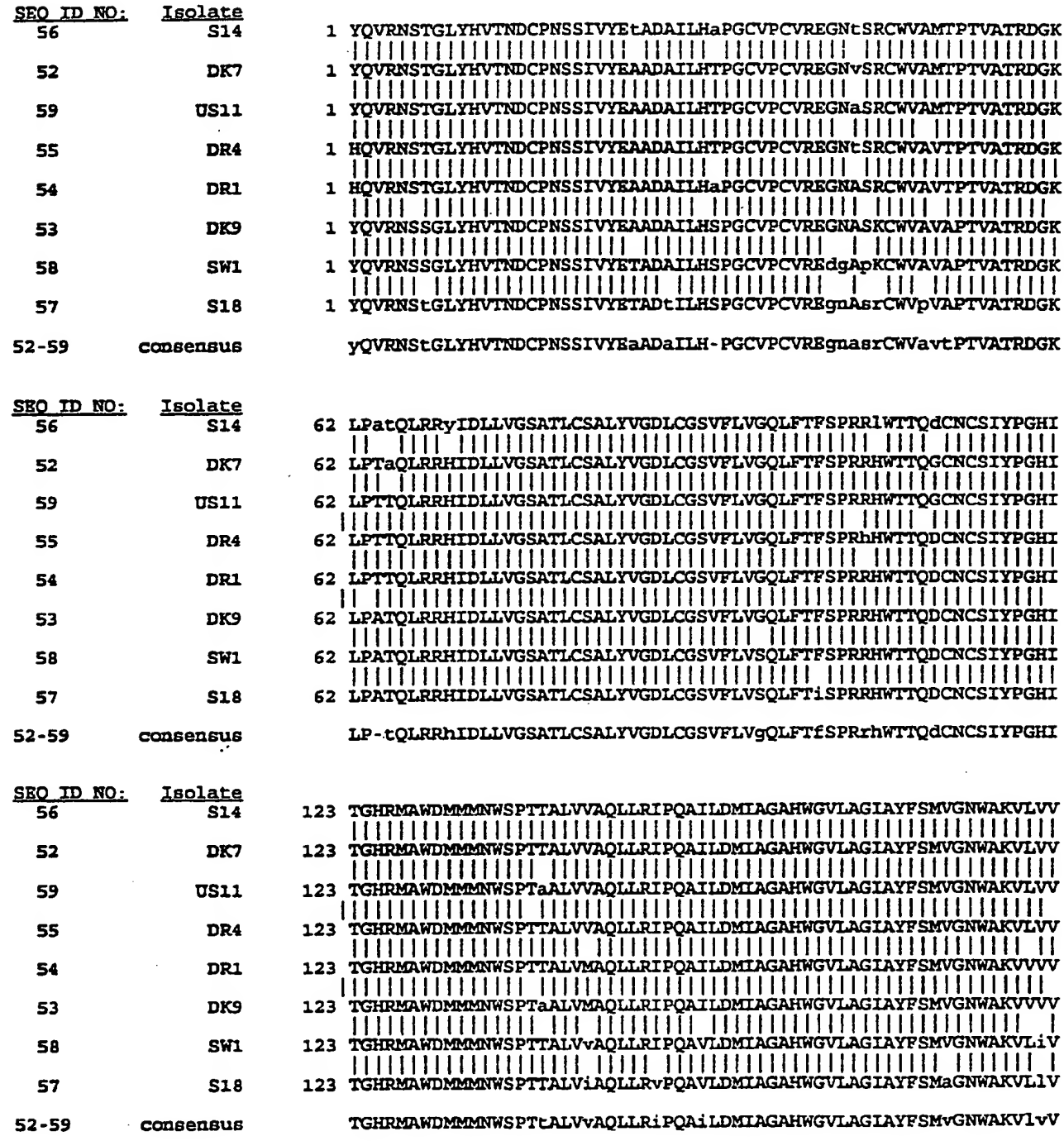
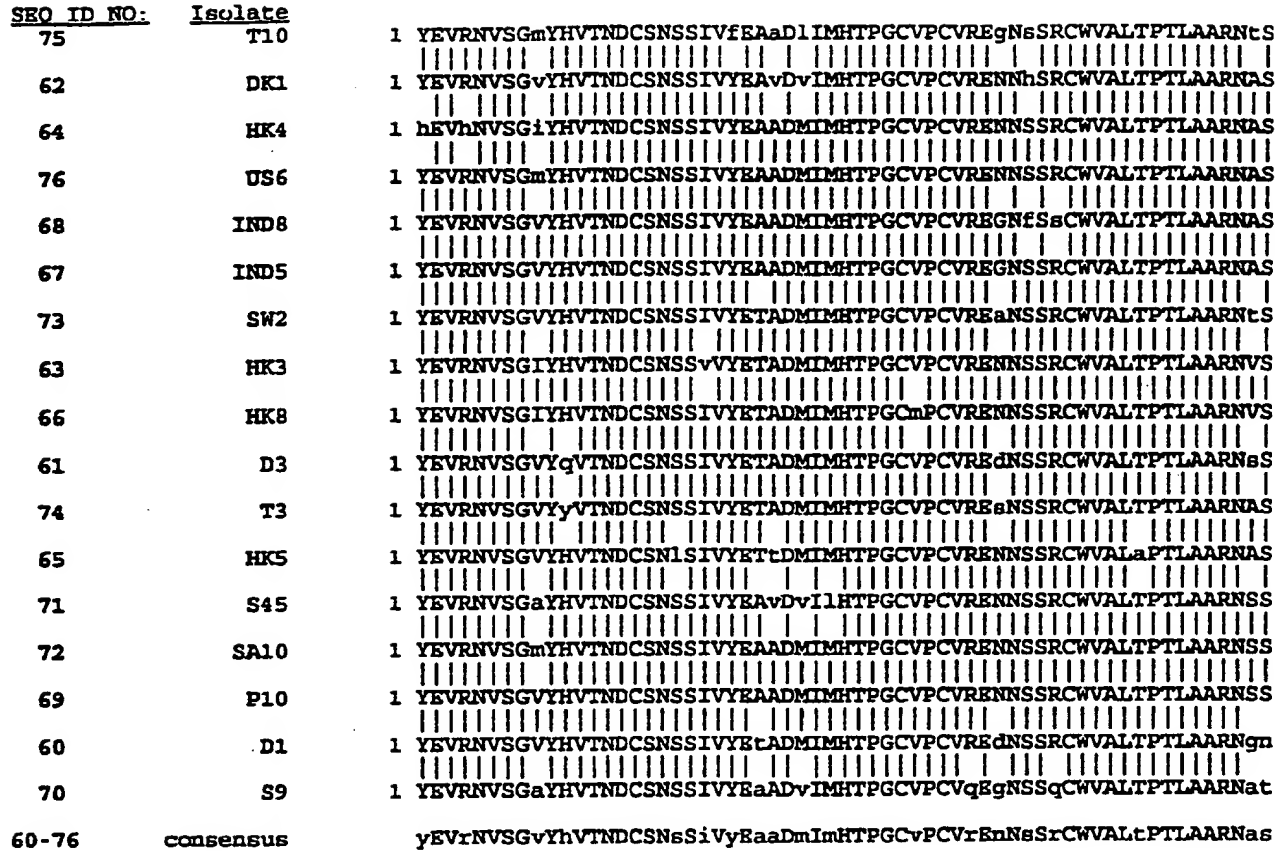

SEQ ID NO: Isolate
56 S14 1 YQVRNSTGLYHVTNDCPNSSIVYEtADAILHaPGCVPCVREGNtSRCWVAMTPTVATRDGK
52 DK7 1 YQVRNSTGLYHVTNDCPNSSIVYEAADAILHTPGCVPCVREGNvSRCWVAMTPTVATRDGK
59 US11 1 YQVRNSTGLYHVTNDCPNSSIVYEAADAILHTPGCVPCVREGNaSRCWVAMTPTVATRDGK
55 DR4 1 HQVRNSTGLYHVTNDCPNSSIVYEAADAILHTPGCVPCVREGNtSRCWVAVTPTVATRDGK
54 DR1 1 HQVRNSTGLYHVTNDCPNSSIVYEAADAILHaPGCVPCVREGNASRCWVAVTPTVATRDGK
53 DK9 1 YQVRNSSGLYHVTNDCPNSSIVYEAADAILHSPGCVPCVREGNASKCWVAVAPTVATRDGK
58 SW1 1 YQVRNSSGLYHVTNDCPNSSIVYETADAILHSPGCVPCVREdgApKCWVAVAPTVATRDGK
57 S18 1 YQVRNStGLYHVTNDCPNSSIVYETADtILHSPGCVPCVREgnAsrCWVpVAPTVATRDGK
52-59 consensus yQVRNStGLYHVTNDCPNSSIVYEaADaILH-PGCVPCVREgnasrCWVavtPTVATRDGK
SEQ ID NO: Isolate
56 S14 62 LPatQLRRyIDLLVGSATLCSALYVGDLCGSVFLVGQLFTFSPRRlWTTQdCNCSIYPGHI
52 DK7 62 LPTaQLRRHIDLLVGSATLCSALYVGDLCGSVFLVGQLFTFSPRRHWTTQGCNCSIYPGHI
59 US11 62 LPTTQLRRHIDLLVGSATLCSALYVGDLCGSVFLVGQLFTFSPRRHWTTQGCNCSIYPGHI
55 DR4 62 LPTTQLRRHIDLLVGSATLCSALYVGDLCGSVFLVGQLFTFSPRhHWTTQDCNCSIYPGHI
54 DR1 62 LPTTQLRRHIDLLVGSATLCSALYVGDLCGSVFLVGQLFTFSPRRHWTTQDCNCSIYPGHI
53 DK9 62 LPATQLRRHIDLLVGSATLCSALYVGDLCGSVFLVGQLFTFSPRRHWTTQDCNCSIYPGHI
58 SW1 62 LPATQLRRHIDLLVGSATLCSALYVGDLCGSVFLVSQLFTFSPRRHWTTQDCNCSIYPGHI
57 S18 62 LPATQLRRHIDLLVGSATLCSALYVGDLCGSVFLVSQLFTiSPRRHWTTQDCNCSIYPGHI
52-59 consensus LP-tQLRRhIDLLVGSATLCSALYVGDLCGSVFLVgQLFTfSPRrhWTTQdCNCSIYPGHI
SEQ ID NO: Isolate
56 S14 123 TGHRMAWDMMMNWSPTTALVVAQLLRIPQAILDMIAGAHWGVLAGIAYFSMVGNWAKVLVV
52 DK7 123 TGHRMAWDMMMNWSPTTALVVAQLLRIPQAILDMIAGAHWGVLAGIAYFSMVGNWAKVLVV
59 US11 123 TGHRMAWDMMMNWSPTaALVVAQLLRIPQAILDMIAGAHWGVLAGIAYFSMVGNWAKVLVV
55 DR4 123 TGHRMAWDMMMNWSPTTALVVAQLLRIPQAILDMIAGAHWGVLAGIAYFSMVGNWAKVLVV
54 DR1 123 TGHRMAWDMMMNWSPTTALVMAQLLRIPQAILDMIAGAHWGVLAGIAYFSMVGNWAKVVVV
53 DK9 123 TGHRMAWDMMMNWSPTaALVMAQLLRIPQAILDMIAGAHWGVLAGIAYFSMVGNWAKVVVV
58 SW1 123 TGHRMAWDMMMNWSPTTALVvAQLLRIPQAVLDMIAGAHWGVLAGIAYFSMVGNWAKVLiV
57 S18 123 TGHRMAWDMMMNWSPTTALViAQLLRvPQAVLDMIAGAHWGVLAGIAYFSMaGNWAKVLlV
52-59 consensus TGHRMAWDMMMNWSPTtALVvAQLLRiPQAiLDMIAGAHWGVLAGIAYFSMvGNWAKVlvV

FIGURE 2A

SEQ ID NO:	Isolate		
56	S14	184	LLLFAGVDA
52	DK7	184	LLLFAGVDA
59	US11	184	LLLFAGVDA
55	DR4	184	LLLFAGVDA
54	DR1	184	LLLFAGVDA
53	DK9	184	LLLFtGVDA
58	SW1	184	LLLFsGVDA
57	S18	184	LLLFaGVDA
52-59	consensus		LLLFaGVDA

FIGURE 2B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62 DK1
64 HK4
76 US6
68 IND8
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72 SA10
69 P10
60 D1
70 S9
60-76 consensus
1 YEVRNVSGmYHVTNDCSNSSIVfEAaDlIMHTPGCVPCVREgNsSRCWVALTPTLAARNtS
1 YEVRNVSGvYHVTNDCSNSSIVYEAvDvIMHTPGCVPCVRENNhSRCWVALTPTLAARNAS
1 hEVhNVSGiYHVTNDCSNSSIVYEAADMIMHTPGCVPCVRENNSSRCWVALTPTLAARNAS
1 YEVRNVSGmYHVTNDCSNSSIVYEAADMIMHTPGCVPCVRENNSSRCWVALTPTLAARNAS
1 YEVRNVSGVYHVTNDCSNSSIVYEAADMIMHTPGCVPCVREGNfSsCWVALTPTLAARNAS
1 YEVRNVSGVYHVTNDCSNSSIVYEAADMIMHTPGCVPCVREGNSSRCWVALTPTLAARNAS
1 YEVRNVSGVYHVTNDCSNSSIVYETADMIMHTPGCVPCVREaNSSRCWVALTPTLAARNtS
1 YEVRNVSGIYHVTNDCSNSSvVYETADMIMHTPGCVPCVRENNSSRCWVALTPTLAARNVS
1 YEVRNVSGIYHVTNDCSNSSIVYETADMIMHTPGCmPCVRENNSSRCWVALTPTLAARNVS
1 YEVRNVSGVYqVTNDCSNSSIVYETADMIMHTPGCVPCVREdNSSRCWVALTPTLAARNsS
1 YEVRNVSGVYyVTNDCSNSSIVYETADMIMHTPGCVPCVREaNSSRCWVALTPTLAARNAS
1 YEVRNVSGVYHVTNDCSNlSIVYETtDMIMHTPGCVPCVRENNSSRCWVALaPTLAARNAS
1 YEVRNVSGaYHVTNDCSNSSIVYEAvDvIlHTPGCVPCVRENNSSRCWVALTPTLAARNSS
1 YEVRNVSGmYHVTNDCSNSSIVYEAADMIMHTPGCVPCVRENNSSRCWVALTPTLAARNSS
1 YEVRNVSGVYHVTNDCSNSSIVYEAADMIMHTPGCVPCVRENNSSRCWVALTPTLAARNSS
1 YEVRNVSGVYHVTNDCSNSSIVYEtADMIMHTPGCVPCVREdNSSRCWVALTPTLAARNgn
1 YEVRNVSGaYHVTNDCSNSSIVYEaADvIMHTPGCVPCVqEgNSSqCWVALTPTLAARNat
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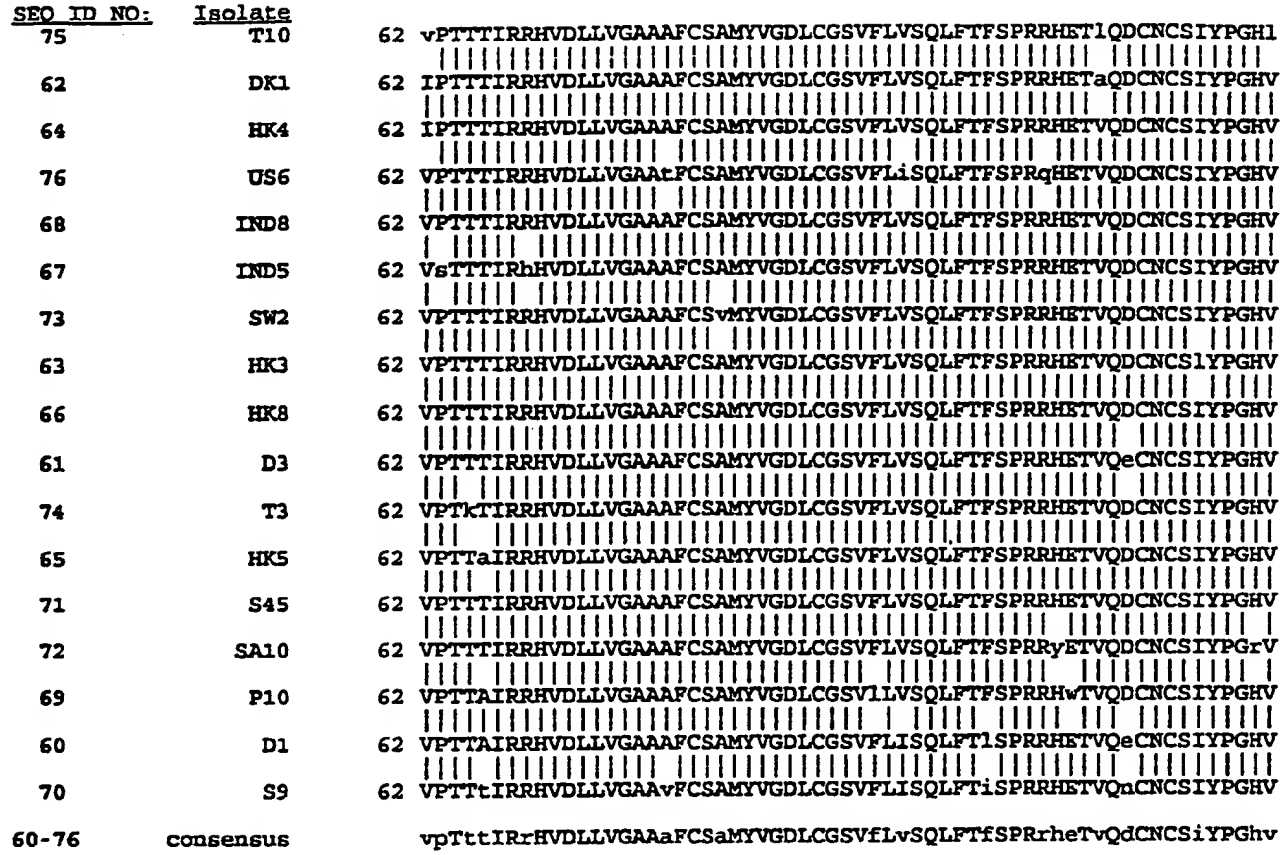
FIGURE 2B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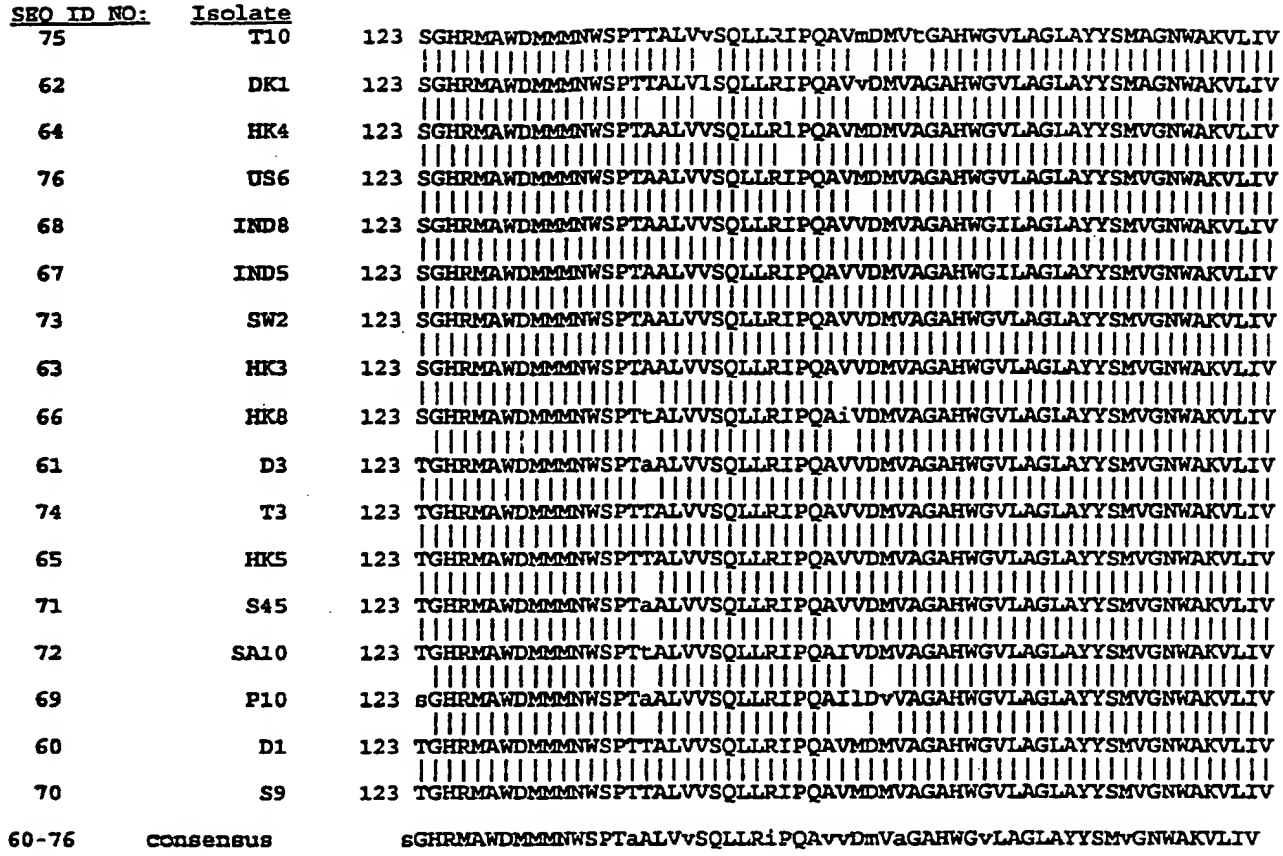
62 DK1 62 IPTTTIRRHVDLLVGAAAFCSAMYVGDLCGSVFLVSQLFTFSPRRHETaQDCNCSIYPGHV
64 HK4 62 IPTTTIRRHVDLLVGAAAFCSAMYVGDLCGSVFLVSQLFTFSPRRHETVQDCNCSIYPGHV
76 US6 62 VPTTTIRRHVDLLVGAAtFCSAMYVGDLCGSVFLiSQLFTFSPRqHETVQDCNCSIYPGHV
68 IND8 62 VPTTTIRRHVDLLVGAAAFCSAMYVGDLCGSVFLVSQLFTFSPRRHETVQDCNCSIYPGHV
67 IND5 62 VsTTTIRhHVDLLVGAAAFCSAMYVGDLCGSVFLVSQLFTFSPRRHETVQDCNCSIYPGHV
73 SW2 62 VPTTTIRRHVDLLVGAAAFCSvMYVGDLCGSVFLVSQLFTFSPRRHETVQDCNCSIYPGHV
63 HK3 62 VPTTTIRRHVDLLVGAAAFCSAMYVGDLCGSVFLVSQLFTFSPRRHETVQDCNCSlYPGHV
66 HK8 62 VPTTTIRRHVDLLVGAAAFCSAMYVGDLCGSVFLVSQLFTFSPRRHETVQDCNCSIYPGHV
61 D3 62 VPTTTIRRHVDLLVGAAAFCSAMYVGDLCGSVFLVSQLFTFSPRRHETVQeCNCSIYPGHV
74 T3 62 VPTkTIRRHVDLLVGAAAFCSAMYVGDLCGSVFLVSQLFTFSPRRHETVQDCNCSIYPGHV
65 HK5 62 VPTTaIRRHVDLLVGAAAFCSAMYVGDLCGSVFLVSQLFTFSPRRHETVQDCNCSIYPGHV
71 S45 62 VPTTTIRRHVDLLVGAAAFCSAMYVGDLCGSVFLVSQLFTFSPRRHETVQDCNCSIYPGHV
72 SA10 62 VPTTTIRRHVDLLVGAAAFCSAMYVGDLCGSVFLVSQLFTFSPRRyETVQDCNCSIYPGrV
69 P10 62 VPTTAIRRHVDLLVGAAAFCSAMYVGDLCGSVlLVSQLFTFSPRRHwTVQDCNCSIYPGHV
60 D1 62 VPTTAIRRHVDLLVGAAAFCSAMYVGDLCGSVFLISQLFTlSPRRHETVQeCNCSIYPGHV
70 S9 62 VPTTtIRRHVDLLVGAAvFCSAMYVGDLCGSVFLISQLFTiSPRRHETVQnCNCSIYPGHV
60-76 consensus vpTttIRrHVDLLVGAAaFCSaMYVGDLCGSVfLvSQLFTfSPRrheTvQdCNCSiYPGhv

FIGURE 2B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75 T10 123 SGHRMAWDMMMNWSPTTALVvSQLLRIPQAVmDMVtGAHWGVLAGLAYYSMAGNWAKVLIV
62 DK1 123 SGHRMAWDMMMNWSPTTALVlSQLLRIPQAVvDMVAGAHWGVLAGLAYYSMAGNWAKVLIV
64 HK4 123 SGHRMAWDMMMNWSPTAALVVSQLLRlPQAVMDMVAGAHWGVLAGLAYYSMVGNWAKVLIV
76 US6 123 SGHRMAWDMMMNWSPTAALVVSQLLRIPQAVMDMVAGAHWGVLAGLAYYSMVGNWAKVLIV
68 IND8 123 SGHRMAWDMMMNWSPTAALVVSQLLRIPQAVVDMVAGAHWGILAGLAYYSMVGNWAKVLIV
67 IND5 123 SGHRMAWDMMMNWSPTAALVVSQLLRIPQAVVDMVAGAHWGILAGLAYYSMVGNWAKVLIV
73 SW2 123 SGHRMAWDMMMNWSPTAALVVSQLLRIPQAVVDMVAGAHWGVLAGLAYYSMVGNWAKVLIV
63 HK3 123 SGHRMAWDMMMNWSPTAALVVSQLLRIPQAVVDMVAGAHWGVLAGLAYYSMVGNWAKVLIV
66 HK8 123 SGHRMAWDMMMNWSPTtALVVSQLLRIPQAiVDMVAGAHWGVLAGLAYYSMVGNWAKVLIV
61 D3 123 TGHRMAWDMMMNWSPTaALVVSQLLRIPQAVVDMVAGAHWGVLAGLAYYSMVGNWAKVLIV
74 T3 123 TGHRMAWDMMMNWSPTTALVVSQLLRIPQAVVDMVAGAHWGVLAGLAYYSMVGNWAKVLIV
65 HK5 123 TGHRMAWDMMMNWSPTTALVVSQLLRIPQAVVDMVAGAHWGVLAGLAYYSMVGNWAKVLIV
71 S45 123 TGHRMAWDMMMNWSPTaALVVSQLLRIPQAVVDMVAGAHWGVLAGLAYYSMVGNWAKVLIV
72 SA10 123 TGHRMAWDMMMNWSPTtALVVSQLLRIPQAIVDMVAGAHWGVLAGLAYYSMVGNWAKVLIV
69 P10 123 sGHRMAWDMMMNWSPTaALVVSQLLRIPQAIlDvVAGAHWGVLAGLAYYSMVGNWAKVLIV
60 D1 123 TGHRMAWDMMMNWSPTTALVVSQLLRIPQAVMDMVAGAHWGVLAGLAYYSMVGNWAKVLIV
70 S9 123 TGHRMAWDMMMNWSPTTALVVSQLLRIPQAVMDMVAGAHWGVLAGLAYYSMVGNWAKVLIV
60-76 consensus sGHRMAWDMMMNWSPTaALVvSQLLRiPQAvvDmVaGAHWGvLAGLAYYSMvGNWAKVLIV

FIGURE 2B

SEQ ID NO:	Isolate		
75	T10	184	mLLFAGVDG
62	DK1	184	lLLFAGVDG
64	HK4	184	mLLFAGVDG
76	US6	184	lLLFAGVDG
68	IND8	184	MLLFAGVDG
67	IND5	184	MLLFAGVDG
73	SW2	184	MLLFAGVDG
63	HK3	184	MLLFAGVDG
66	HK8	184	MLLFAGVDG
61	D3	184	MLLFAGVDG
74	T3	184	lLLFAGVDG
65	HK5	184	MLLFAGVDG
71	S45	184	MLLFAGVDG
72	SA10	184	MLLFAGVDG
69	P10	184	MLLFAGVDG
60	D1	184	MLLFAGVDG
70	S9	184	MLLFAGVDG
60-76	consensus		mLLFAGVDG

FIGURE 2C

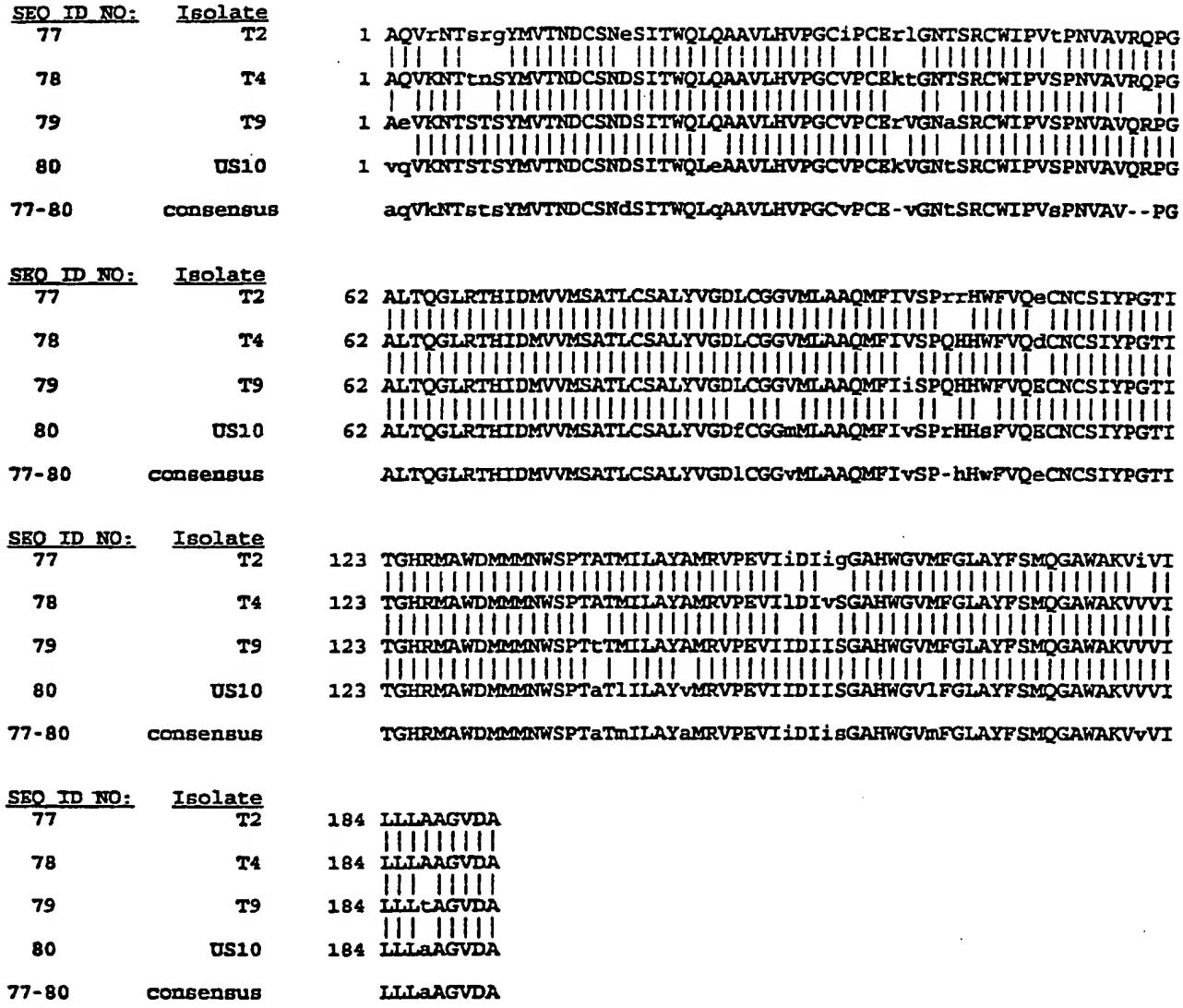

SEQ ID NO: Isolate
77 T2 1 AQVrNTsrgYMVTNDCSNeSITWQLQAAVLHVPGCiPCErlGNTSRCWIPVtPNVAVRQPG
78 T4 1 AQVKNTtnSYMVTNDCSNDSITWQLQAAVLHVPGCVPCEktGNTSRCWIPVSPNVAVRQPG
79 T9 1 AeVKNTSTSYMVTNDCSNDSITWQLQAAVLHVPGCVPCErVGNaSRCWIPVSPNVAVQRPG
80 US10 1 vqVKNTSTSYMVTNDCSNDSITWQLeAAVLHVPGCVPCEkVGNtSRCWIPVSPNVAVQRPG
77-80 consensus aqVkNTstsYMVTNDCSNdSITWQLqAAVLHVPGCvPCE-vGNtSRCWIPVsPNVAV--PG
SEQ ID NO: Isolate
77 T2 62 ALTQGLRTHIDMVVMSATLCSALYVGDLCGGVMLAAQMFIVSPrrHWFVQeCNCSIYPGTI
78 T4 62 ALTQGLRTHIDMVVMSATLCSALYVGDLCGGVMLAAQMFIVSPQHHWFVQdCNCSIYPGTI
79 T9 62 ALTQGLRTHIDMVVMSATLCSALYVGDLCGGVMLAAQMFIiSPQHHWFVQECNCSIYPGTI
80 US10 62 ALTQGLRTHIDMVVMSATLCSALYVGDfCGGmMLAAQMFIvSPrHHsFVQECNCSIYPGTI
77-80 consensus ALTQGLRTHIDMVVMSATLCSALYVGDlCGGvMLAAQMFIvSP-hHwFVQeCNCSIYPGTI
SEQ ID NO: Isolate
77 T2 123 TGHRMAWDMMMNWSPTATMILAYAMRVPEVIiDIigGAHWGVMFGLAYFSMQGAWAKViVI
78 T4 123 TGHRMAWDMMMNWSPTATMILAYAMRVPEVIlDIvSGAHWGVMFGLAYFSMQGAWAKVVVI
79 T9 123 TGHRMAWDMMMNWSPTtTMILAYAMRVPEVIIDIISGAHWGVMFGLAYPSMQGAWAKVVVI
80 US10 123 TGHRMAWDMMMNWSPTaTlILAYvMRVPEVIIDIISGAHWGVlFGLAYFSMQGAWAKVVVI
77-80 consensus TGHRMAWDMMMNWSPTaTmILAYaMRVPEVIiDIisGAHWGVmFGLAYFSMQGAWAKVvVI
SEQ ID NO: Isolate
77 T2 184 LLLAAGVDA
78 T4 184 LLLAAGVDA
79 T9 184 LLLtAGVDA
80 US10 184 LLLaAGVDA
77-80 consensus LLLaAGVDA

FIGURE 2D

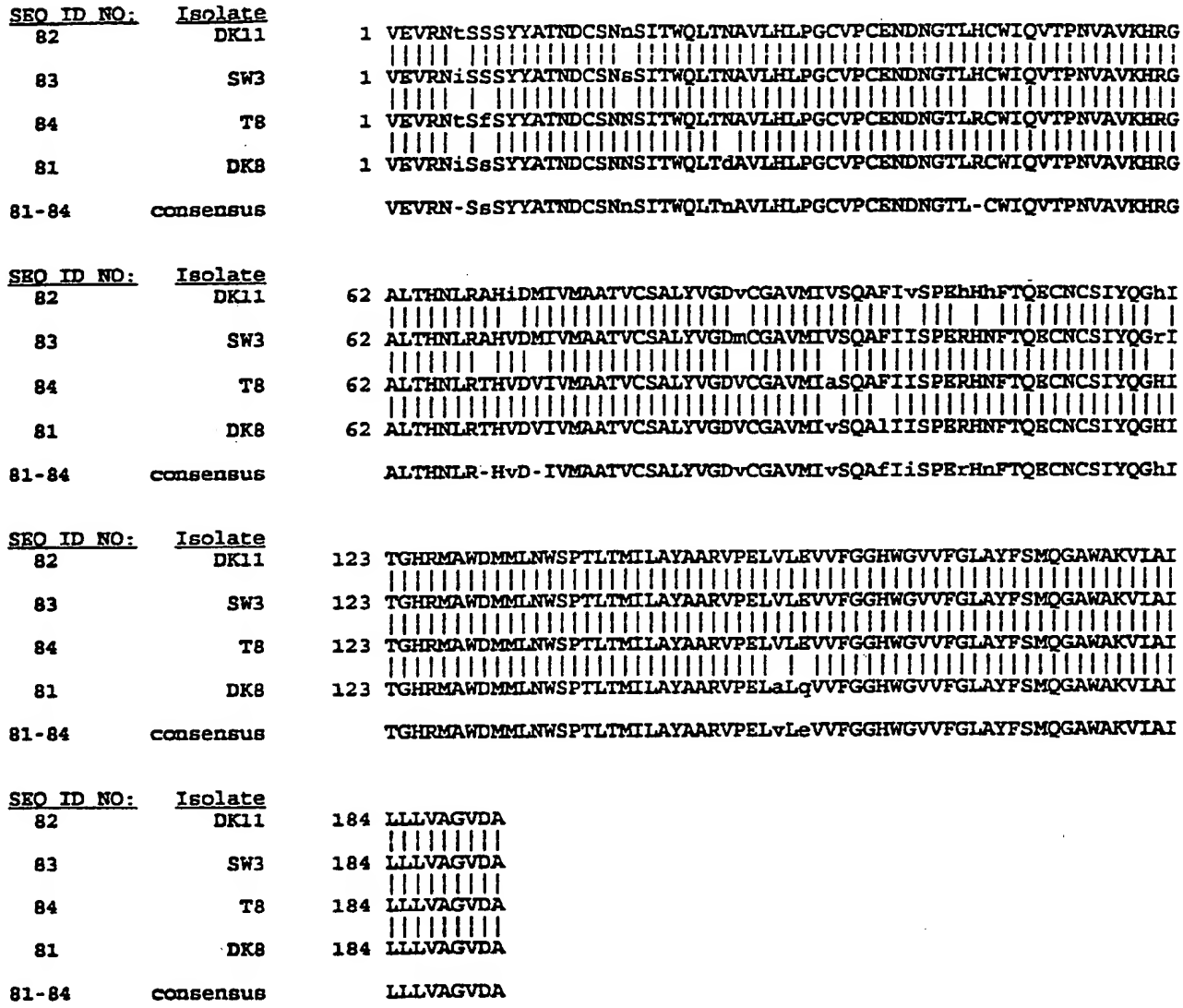
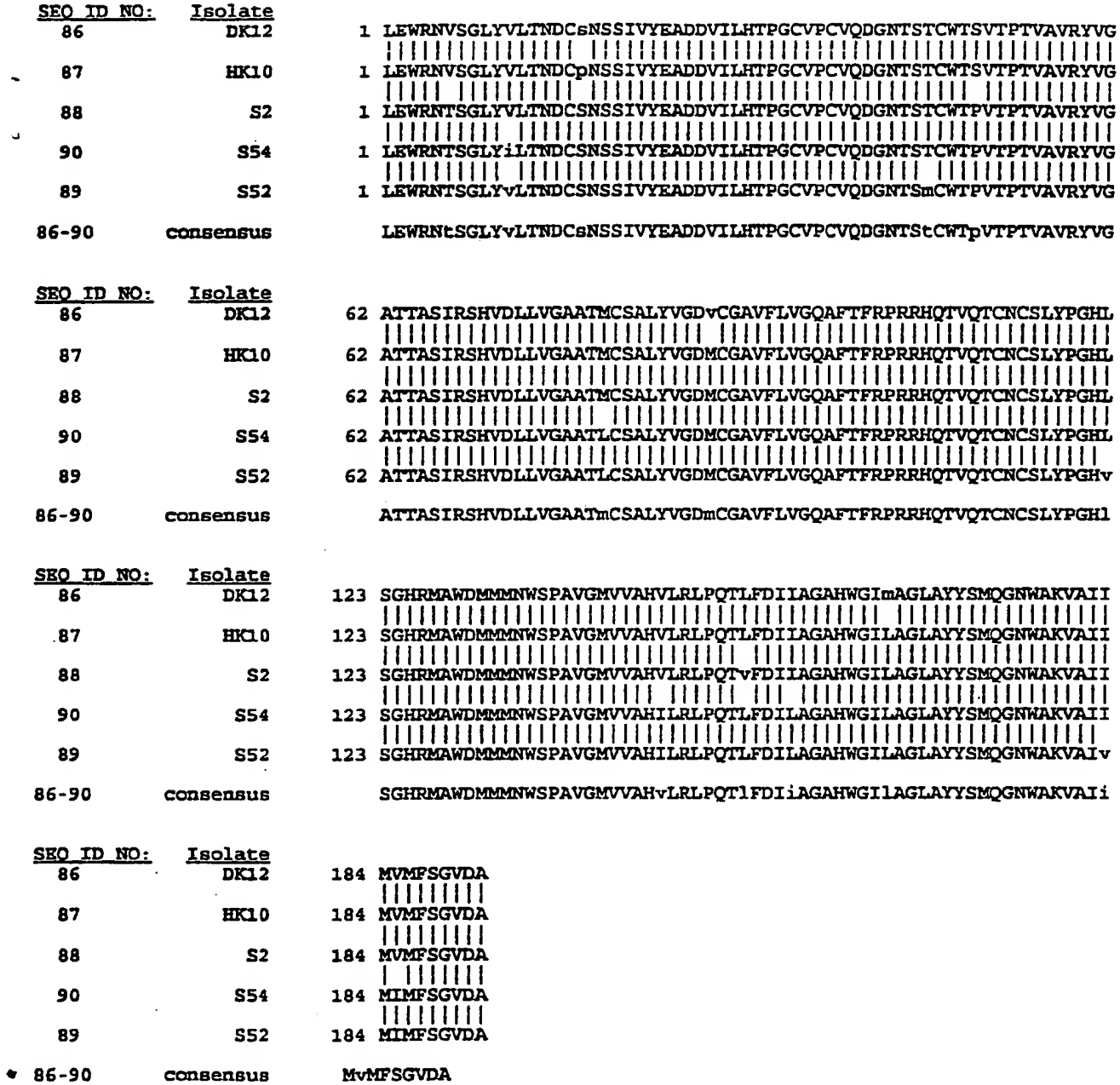

SEQ ID NO: Isolate
82 DK11 1 VEVRNtSSSYYATNDCSNnSITWQLTNAVLHLPGCVPCENDNGTLHCWIQVTPNVAVKHRG
83 SW3 1 VEVRNiSSSYYATNDCSNsSITWQLTNAVLHLPGCVPCENDNGTLHCWIQVTPNVAVKHRG
84 T8 1 VEVRNtSfSYYATNDCSNNSITWQLTNAVLHLPGCVPCENDNGTLRCWIQVTPNVAVKHRG
81 DK8 1 VEVRNiSsSYYATNDCSNNSITWQLTdAVLHLPGCVPCENDNGTLRCWIQVTPNVAVKHRG
81-84 consensus VEVRN-SsSYYATNDCSNnSITWQLTnAVLHLPGCVPCENDNGTL-CWIQVTPNVAVKHRG
SEQ ID NO: Isolate
82 DK11 62 ALTHNLRAHiDMIVMAATVCSALYVGDvCGAVMIVSQAFIvSPEhHhFTQECNCSIYQGhI
83 SW3 62 ALTHNLRAHVDMIVMAATVCSALYVGDmCGAVMIVSQAFIISPERHNFTQECNCSIYQGrI
84 T8 62 ALTHNLRTHVDVIVMAATVCSALYVGDVCGAVMIaSQAFIISPERHNFTQECNCSIYQGHI
81 DK8 62 ALTHNLRTHVDVIVMAATVCSALYVGDVCGAVMIvSQAlIISPERHNFTQECNCSIYQGHI
81-84 consensus ALTHNLR-HvD-IVMAATVCSALYVGDvCGAVMIvSQAfIiSPErHnFTQECNCSIYQGhI
SEQ ID NO: Isolate
82 DK11 123 TGHRMAWDMMLNWSPTLTMILAYAARVPELVLEVVFGGHWGVVFGLAYFSMQGAWAKVIAI
83 SW3 123 TGHRMAWDMMLNWSPTLTMILAYAARVPELVLEVVFGGHWGVVFGLAYFSMQGAWAKVIAI
84 T8 123 TGHRMAWDMMLNWSPTLTMILAYAARVPELVLEVVFGGHWGVVFGLAYFSMQGAWAKVIAI
81 DK8 123 TGHRMAWDMMLNWSPTLTMILAYAARVPELaLqVVFGGHWGVVFGLAYFSMQGAWAKVIAI
81-84 consensus TGHRMAWDMMLNWSPTLTMILAYAARVPELvLeVVFGGHWGVVFGLAYFSMQGAWAKVIAI
SEQ ID NO: Isolate
82 DK11 184 LLLVAGVDA
83 SW3 184 LLLVAGVDA
84 T8 184 LLLVAGVDA
81 DK8 184 LLLVAGVDA
81-84 consensus LLLVAGVDA

FIGURE 2E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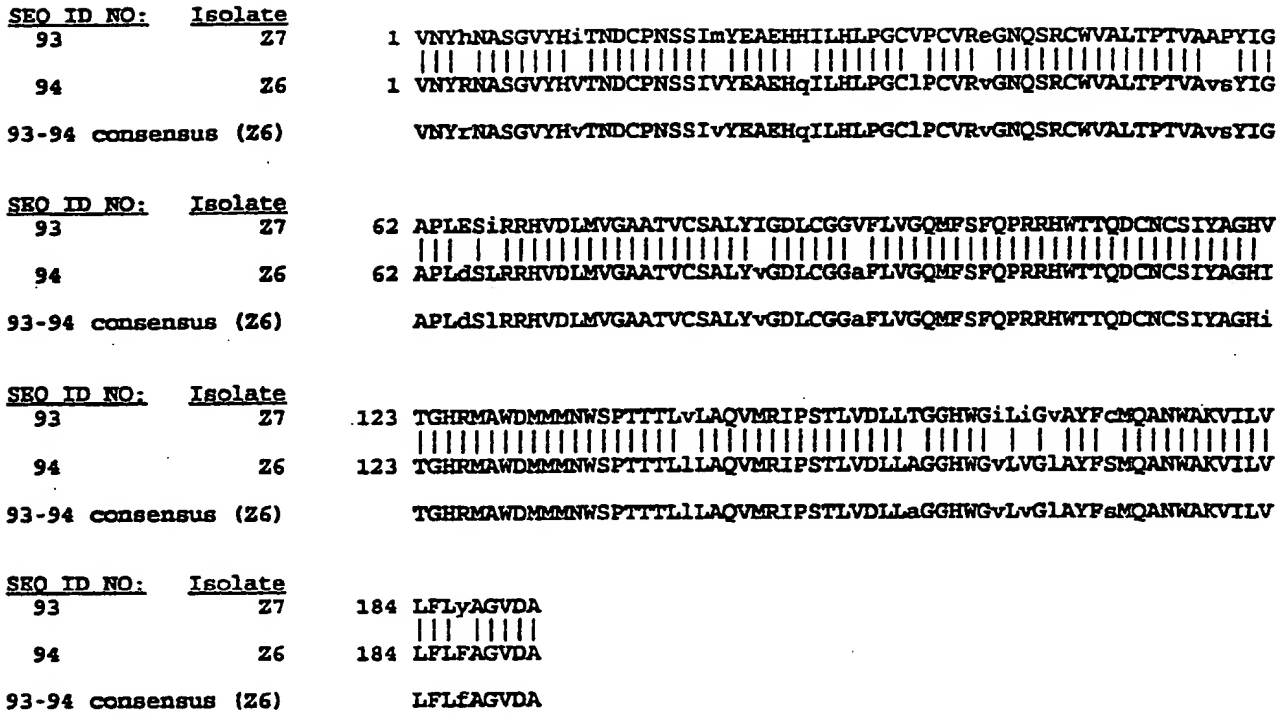
87 HK10 1 LEWRNVSGLYVLTNDCpNSSIVYEADDVILHTPGCVPCVQDGNTSTCWTSVTPTVAVRYVG
88 S2 1 LEWRNTSGLYVLTNDCSNSSIVYEADDVILHTPGCVPCVQDGNTSTCWTPVTPTVAVRYVG
90 S54 1 LEWRNTSGLYiLTNDCSNSSIVYEADDVILHTPGCVPCVQDGNTSTCWTPVTPTVAVRYVG
89 S52 1 LEWRNTSGLYvLTNDCSNSSIVYEADDVILHTPGCVPCVQDGNTSmCWTPVTPTVAVRYVG
86-90 consensus LEWRNtSGLYvLTNDCsNSSIVYEADDVILHTPGCVPCVQDGNTStCWTpVTPTVAVRYVG
SEQ ID NO: Isolate
86 DK12 62 ATTASIRSHVDLLVGAATMCSALYVGDvCGAVFLVGQAFTFRPRRHQTVQTCNCSLYPGHL
87 HK10 62 ATTASIRSHVDLLVGAATMCSALYVGDMCGAVFLVGQAFTFRPRRHQTVQTCNCSLYPGHL
88 S2 62 ATTASIRSHVDLLVGAATMCSALYVGDMCGAVFLVGQAFTFRPRRHQTVQTCNCSLYPGHL
90 S54 62 ATTASIRSHVDLLVGAATLCSALYVGDMCGAVFLVGQAFTFRPRRHQTVQTCNCSLYPGHL
89 S52 62 ATTASIRSHVDLLVGAATLCSALYVGDMCGAVFLVGQAFTFRPRRHQTVQTCNCSLYPGHv
86-90 consensus ATTASIRSHVDLLVGAATmCSALYVGDmCGAVFLVGQAFTFRPRRHQTVQTCNCSLYPGHl
SEQ ID NO: Isolate
86 DK12 123 SGHRMAWDMMMNWSPAVGMVVAHVLRLPQTLFDIIAGAHWGImAGLAYYSMQGNWAKVAII
87 HK10 123 SGHRMAWDMMMNWSPAVGMVVAHVLRLPQTLFDIIAGAHWGILAGLAYYSMQGNWAKVAII
88 S2 123 SGHRMAWDMMMNWSPAVGMVVAHVLRLPQTvFDIIAGAHWGILAGLAYYSMQGNWAKVAII
90 S54 123 SGHRMAWDMMMNWSPAVGMVVAHILRLPQTLFDILAGAHWGILAGLAYYSMQGNWAKVAII
89 S52 123 SGHRMAWDMMMNWSPAVGMVVAHILRLPQTLFDILAGAHWGILAGLAYYSMQGNWAKVAIv
86-90 consensus SGHRMAWDMMMNWSPAVGMVVAHvLRLPQTlFDIiAGAHWGIlAGLAYYSMQGNWAKVAIi
SEQ ID NO: Isolate
86 DK12 184 MVMFSGVDA
87 HK10 184 MVMFSGVDA
88 S2 184 MVMFSGVDA
90 S54 184 MIMFSGVDA
89 S52 184 MIMFSGVDA
86-90 consensus MvMFSGVDA

FIGURE 2F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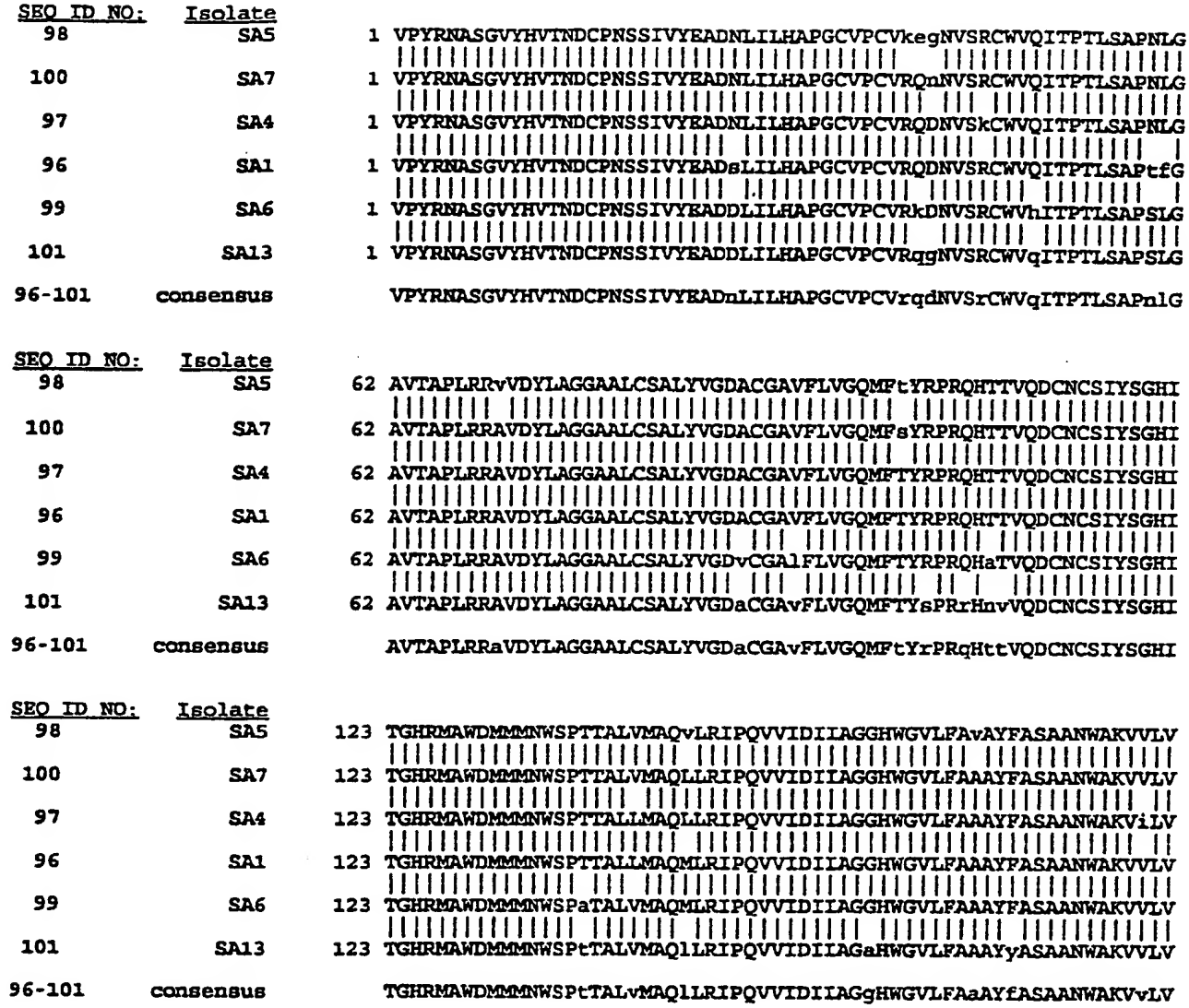
93 Z7 1 VNYhNASGVYHiTNDCPNSSImYEAEHHILHLPGCVPCVReGNQSRCWVALTPTVAAPYIG
94 Z6 1 VNYRNASGVYHVTNDCPNSSIVYEAEHqILHLPGClPCVRvGNQSRCWVALTPTVAvsYIG
93-94 consensus (Z6) VNYrNASGVYHvTNDCPNSSIvYEAEHqILHLPGClPCVRvGNQSRCWVALTPTVAvsYIG
SEQ ID NO: Isolate
93 Z7 62 APLESiRRHVDLMVGAATVCSALYIGDLCGGVFLVGQMFSFQPRRHWTTQDCNCSIYAGHV
94 Z6 62 APLdSLRRHVDLMVGAATVCSALYvGDLCGGaFLVGQMFSFQPRRHWTTQDCNCSIYAGHI
93-94 consensus (Z6) APLdSlRRHVDLMVGAATVCSALYvGDLCGGaFLVGQMFSFQPRRHWTTQDCNCSIYAGHi
SEQ ID NO: Isolate
93 Z7 123 TGHRMAWDMMMNWSPTTTLvLAQVMRIPSTLVDLLTGGHWGiLiGvAYFcMQANWAKVILV
94 Z6 123 TGHRMAWDMMMNWSPTTTLlLAQVMRIPSTLVDLLAGGHWGvLVGlAYFSMQANWAKVILV
93-94 consensus (Z6) TGHRMAWDMMMNWSPTTTLlLAQVMRIPSTLVDLLaGGHWGvLvGlAYFsMQANWAKVILV
SEQ ID NO: Isolate
93 Z7 184 LFLyAGVDA
94 Z6 184 LFLFAGVDA
93-94 consensus (Z6) LFLfAGVDA

FIGURE 2G


SEQ ID NO: Isolate
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100 SA7 1 VPYRNASGVYHVTNDCPNSSIVYEADNLILHAPGCVPCVRQnNVSRCWVQITPTLSAPNLG
97 SA4 1 VPYRNASGVYHVTNDCPNSSIVYEADNLILHAPGCVPCVRQDNVSkCWVQITPTLSAPNLG
96 SA1 1 VPYRNASGVYHVTNDCPNSSIVYEADsLILHAPGCVPCVRQDNVSRCWVQITPTLSAPtfG
99 SA6 1 VPYRNASGVYHVTNDCPNSSIVYEADDLILHAPGCVPCVRkDNVSRCWVhITPTLSAPSLG
101 SA13 1 VPYRNASGVYHVTNDCPNSSIVYEADDLILHAPGCVPCVRqgNVSRCWVqITPTLSAPSLG
96-101 consensus VPYRNASGVYHVTNDCPNSSIVYEADnLILHAPGCVPCVrqdNVSrCWVqITPTLSAPnlG
SEQ ID NO: Isolate
98 SA5 62 AVTAPLRRvVDYLAGGAALCSALYVGDACGAVFLVGQMFtYRPRQHTTVQDCNCSIYSGHI
100 SA7 62 AVTAPLRRAVDYLAGGAALCSALYVGDACGAVFLVGQMFsYRPRQHTTVQDCNCSIYSGHI
97 SA4 62 AVTAPLRRAVDYLAGGAALCSALYVGDACGAVFLVGQMFTYRPRQHTTVQDCNCSIYSGHI
96 SA1 62 AVTAPLRRAVDYLAGGAALCSALYVGDACGAVFLVGQMFTYRPRQHTTVQDCNCSIYSGHI
99 SA6 62 AVTAPLRRAVDYLAGGAALCSALYVGDvCGAlFLVGQMFTYRPRQHaTVQDCNCSIYSGHI
101 SA13 62 AVTAPLRRAVDYLAGGAALCSALYVGDaCGAvFLVGQMFTYsPRrHnvVQDCNCSIYSGHI
96-101 consensus AVTAPLRRaVDYLAGGAALCSALYVGDaCGAvFLVGQMFtYrPRqHttVQDCNCSIYSGHI
SEQ ID NO: Isolate
98 SA5 123 TGHRMAWDMMMNWSPTTALVMAQvLRIPQVVIDIIAGGHWGVLFAvAYFASAANWAKVVLV
100 SA7 123 TGHRMAWDMMMNWSPTTALVMAQLLRIPQVVIDIIAGGHWGVLFAAAYFASAANWAKVVLV
97 SA4 123 TGHRMAWDMMMNWSPTTALLMAQLLRIPQVVIDIIAGGHWGVLFAAAYFASAANWAKViLV
96 SA1 123 TGHRMAWDMMMNWSPTTALLMAQMLRIPQVVIDIIAGGHWGVLFAAAYFASAANWAKVVLV
99 SA6 123 TGHRMAWDMMMNWSPaTALVMAQMLRIPQVVIDIIAGGHWGVLFAAAYFASAANWAKVVLV
101 SA13 123 TGHRMAWDMMMNWSPtTALVMAQlLRIPQVVIDIIAGaHWGVLFAAAYyASAANWAKVVLV
96-101 consensus TGHRMAWDMMMNWSPtTALvMAQlLRIPQVVIDIIAGgHWGVLFAaAYfASAANWAKVvLV

FIGURE 2G

SEQ ID NO:	Isolate		
98	SA5	184	LFLFAGVDg
100	SA7	184	LFLFAGVDA
97	SA4	184	LFLFAGVDA
96	SA1	184	LFLFAGVDg
99	SA6	184	LFLFAGVDA
101	SA13	184	LFLFAGVDA
96-101	consensus		LFLFAGVDa

FIGURE 2H

SEQ ID NO:	Genotype		
81-84	(IV/2b)	1	VEVRNiSsSYYATNDCSNnSITWQLTnAVLHLPGCVPCENDNGTLrCWIQVTPNVAVKHRG
85	(2c)	1	VEVKDTGDSYMPTNDCSNSSIVWQLEGAVLHTPGCVPCERTANVSRCWVPVAPNLAISQPG
77-80	(III/2a)	1	aqVkNTstsYMVTNDCSNdSITWQLqAAVLHVPGCvPCEkvGNtSRCWIPVsPNVAVqqPG
86-90	(V/3a)	1	LEWRNtSGLYvLTNDCsNSSIVYEADDVILHTPGCVPCVQDGNTStCWIpVTPTVAVRYVG
60-76	(II/1b)	1	yEVrNVSGvYhVTNDCSNsSiVyEaaDmImHTPGCvPCVrEnNsSrCWVALtPTLAARNas
52-59	(I/1a)	1	yQVRNStGLYHVTNDCPNSSIVYEaADaILHsPGCVPCVREgnasrCWVavtPTVATRDGK
91	(4a)	1	EHYRNASGIYHITNDCPNSSIVYEADHHILHLPGCVPCVMTGNTSRCWTPVTPTVAVAHPG
93-94	(4c)	1	VNYrNASGVYHvTNDCPNSSIvYEAEHqILHLPGClPCVRvGNQSRCWVALTPTVAvsYIG
95	(4d)	1	YNYRNSSGVYHVTNDCPNSSIVYETDYHILHLPGCVPCVREGNKSTCWVSLTPTVAAQHLN
92	(4b)	1	VHYRNASGVYHVTNDCPNTSIVYETEHHIMHLPGCVPCVRTENTSRCWVPLTPTVAAPYPN
96-101	(5a)	1	VPYRNASGVYHVTNDCPNSSIVYEADnLILHAPGCVPCVrqdNVSrCWVqITPTLSAPnlG
102	(6a)	1	LTYGNSSGLYHLTNDCPNSSIVLEADAMILHLPGCLPCVRVDDRSTCWHAVTPTLAIPNAS
52-102	consensus		Y TNDC N S H PGC PC CW P

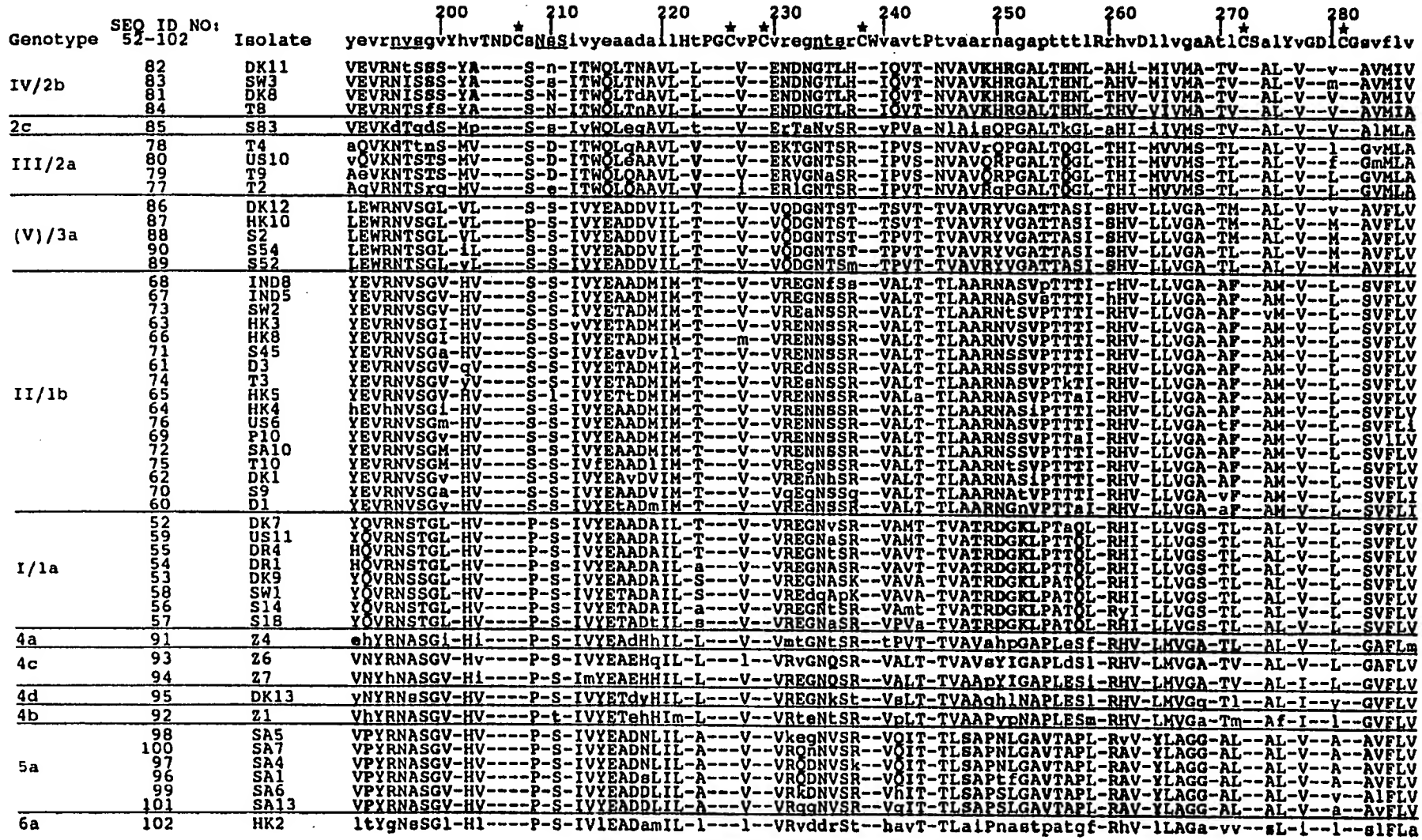
SEQ ID NO:	Genotype		
81-84	(IV/2b)	62	ALTHNLRtHvDmIVMAATVCSALYVGDvCGAVMIvSQAfIiSPErHnFTQECNCSIYQGhI
85	(2c)	62	ALTKGLRAHIDIIVMSATVCSALYVGDVCGALMLAAQVVVVSPQHHTFVQECNCSIYPGRI
77-80	(III/2a)	62	ALTQGLRTHIDMVVMSATLCSALYVGDlCGGvMLAAQMFIvSPqhHwFVQeCNCSIYPGTI
86-90	(V/3a)	62	ATTASIRSHVDLLVGAATmCSALYVGDmCGAVFLVGQAFTFRPRRHQTVQTCNCSLYPGHl
60-76	(II/1b)	62	vpTttIRrHVDLLVGAAaFCSaMYVGDLCGSVfLvSQLFTfSPRrheTvQdCNCSiYPGhv
52-59	(I/1a)	62	LPatQLRRhIDLLVGSATLCSALYVGDLCGSVFLVgQLFTfSPRrhWTTQdCNCSIYPGHI
91	(4a)	62	APLESFRRHVDLMVGAATLCSALYVGDLCGGAFLMGQMITFRPRRHWTTQECNCSIYTGHI
93-94	(4c)	62	APLdSlRRHVDLMVGAATVCSALYvGDLCGGaFLVGQMFSFQPRRHWTTQDCNCSIYAGHi
95	(4d)	62	APLESLRRHVDLMVGGATLCSALYIGDVCGGVFLVGQLFTFQPRRHWTTQDCNCSIYTGHI
92	(4b)	62	APLESMRRHVDLMVGAATMCSAFYIGDLCGGVFLVGQLFDFRPRRHWTTQDCNCSIYPGHV
96-101	(5a)	62	AVTAPLRRaVDYLAGGAALCSALYVGDaCGAvFLVGQMFtYrPRqHttVQDCNCSIYSGHI
102	(6a)	62	TPATGFRRHVDLLAGAAVVCSSLYIGDLCGSLFLAGQLFTFQPRRHWTVQDCNCSIYTGHV
52-102	consensus		R D A CS Y GD CG Q P Q CNCS Y G

SEQ ID NO:	Genotype		
81-84	(IV/2b)	123	TGHRMAWDMMLNWSPTLTMILAYAARVPELvLeVVFGGHWGVVFGLAYFSMQGAWAKVIAI
85	(2c)	123	TGHRMAWDMMMNWSPTTTMLLAYLVRIPEVILDIVTGGHWGVMFGLAYFSMQGSWAKVIVI
77-80	(III/2a)	123	TGHRMAWDMMMNWSPTaTmILAYaMRVPEVIiDIisGAHWGVmFGLAYFSMQGAWAKVvVI
86-90	(V/3a)	123	SGHRMAWDMMMNWSPAVGMVVAHvLRLPQTlFDIiAGAHWGIlAGLAYYSMQGNWAKVAIi
60-76	(II/1b)	123	sGHRMAWDMMMNWSPTaALVvSQLLRiPQAvvDmVaGAHWGvLAGLAYYSMvGNWAKVLIV
52-59	(I/1a)	123	TGHRMAWDMMMNWSPTtALVvAQLLRiPQAiLDMIAGAHWGVLAGIAYFSMvGNWAKVlvV
91	(4a)	123	TGHRMAWDMMMNWSPTTTLLLAQIMRVPTAFLDMVAGGHWGVLAGLAYFSMQGNWAKVVLV
93-94	(4c)	123	TGHRMAWDMMMNWSPTTTLlLAQVMRIPSTLVDLLaGGHWGvLvGlAYFsMQANWAKVILV
95	(4d)	123	TGHRMAWDMMMNWSPTATLVLAQLMRIPGAMVDLLAGGHWGILVGIAYFSMQANWAKVILV
92	(4b)	123	SGHRMAWDMMMNWSPTSALIMAQILRIPSILGDLLTGGHWGVLAGLAFFSMQSNWAKVILV
96-101	(5a)	123	TGHRMAWDMMMNWSPtTALvMAQlLRIPQVVIDIIAGgHWGVLFAaAYfASAANWAKVvLV
102	(6a)	123	TGHRMAWDMMMNWSPTTTLVLSSILRVPEICASVIFGGHWGILLAVAYFGMAGNWLKVLAV
52-102	consenus		GHRMAWDMM NWSP R P G HWG A W KV

FIGURE 2H

SEQ ID NO:	Genotype		
81-84	(IV/2b)	184	LLLVAGVDA
85	(2c)	184	LLLTAGVEA
77-80	(III/2a)	184	LLLaAGVDA
86-90	(V/3a)	184	MvMFSGVDA
60-76	(II/1b)	184	mLLFAGVDG
52-59	(I/1a)	184	LLLFaGVDA
91	(4a)	184	LFLFAGVDA
93-94	(4c)	184	LFLfAGVDA
95	(4d)	184	LFLFAGVDA
92	(4b)	184	LFLFAGVEG
96-101	(5a)	184	LFLFAGVDa
102	(6a)	184	LFLFAGVEA
52-102	consensus		GV

FIGURE 3


SEQ ID NO:
Genotype 52-102 Isolate
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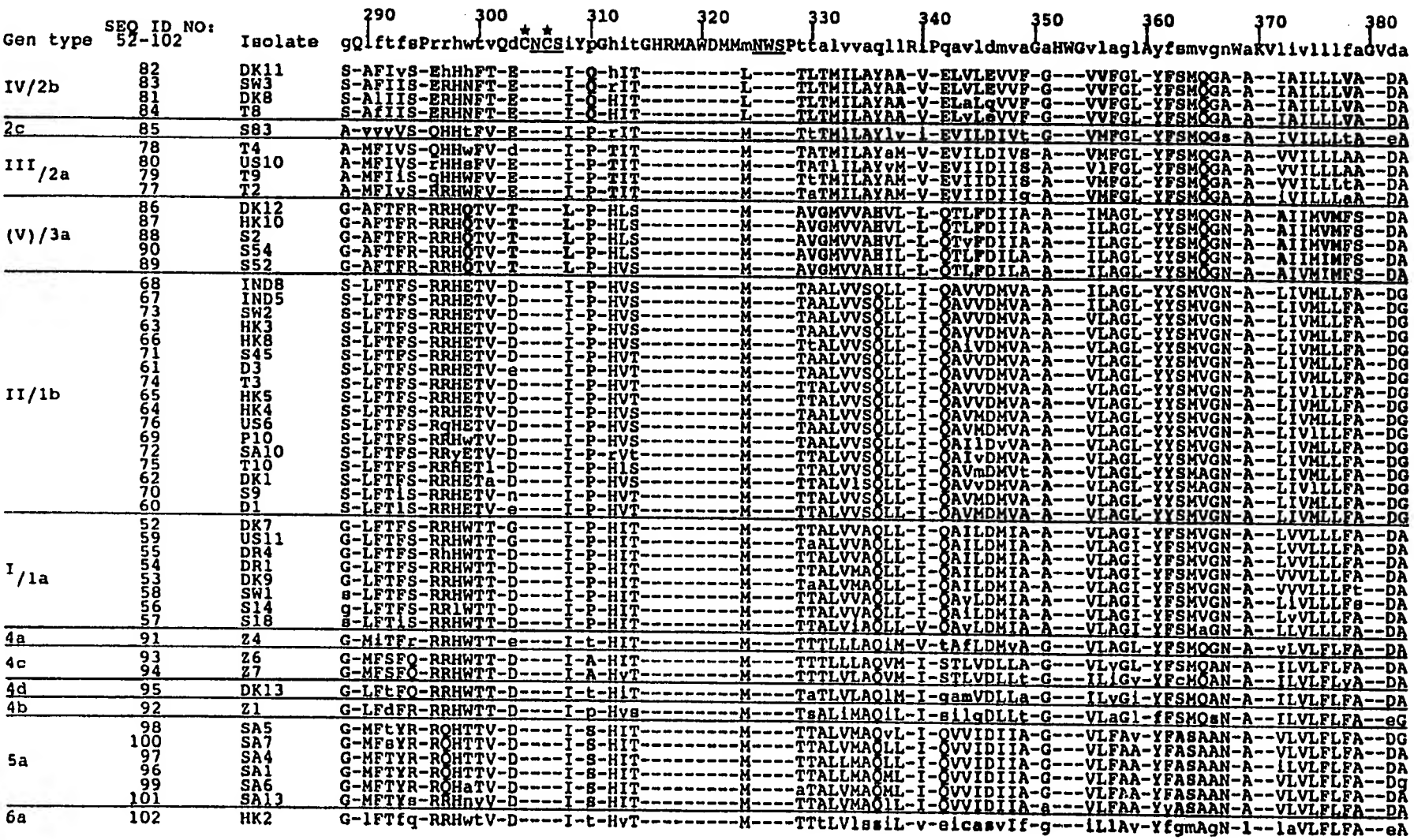
IV/2b 82 DK11 VEVRNtSSS-YA----S-n-ITWQLTNAVL-L---V--ENDNGTLH--IQVT-NVAVKHRGALTHNL-AHi-MIVMA-TV--AL-V--v--AVMIV
83 SW3 VEVRNISSS-YA----S-s-ITWQLTNAVL-L---V--ENDNGTLH--IQVT-NVAVKHRGALTHNL-AHV-MIVMA-TV--AL-V--m--AVMIV
81 DK8 VEVRNISSS-YA----S-N-ITWQLTdAVL-L---V--ENDNGTLR--IQVT-NVAVKHRGALTHNL-THV-VIVMA-TV--AL-V--V--AVMIV
84 T8 VEVRNTSfS-YA----S-N-ITWQLTnAVL-L---V--ENDNGTLR--IQVT-NVAVKHRGALTHNL-THV-VIVMA-TV--AL-V--V--AVMIA
2c 85 S83 VEVKdTqdS-Mp----S-s-IvWQLeqAVL-t---V--ErTaNvSR--vPVa-NlAisQPGALTkGL-aHI-iIVMS-TV--AL-V--V--AlMLA
III/2a 78 T4 aQVKNTtnS-MV----S-D-ITWQLqAAVL-V---V--EKTGNTSR--IPVS-NVAVrQPGALTQGL-THI-MVVMS-TL--AL-V--l--GvMLA
80 US10 vQVKNTSTS-MV----S-D-ITWQLeAAVL-V---V--EKVGNTSR--IPVS-NVAVQRPGALTQGL-THI-MVVMS-TL--AL-V--f--GmMLA
79 T9 AeVKNTSTS-MV----S-D-ITWQLQAAVL-V---V--ERVGNaSR--IPVS-NVAVQRPGALTQGL-THI-MVVMS-TL--AL-V--L--GVMLA
77 T2 AqVRNTSrq-MV----S-e-ITWQLQAAVL-V---i--ERIGNTSR--IPVT-NVAVRqPGALTQGL-THI-MVVMS-TL--AL-V--L--GVMLA
(V)/3a 86 DK12 LEWRNVSGL-VL----S-S-IVYEADDVIL-T---V--VQDGNTST--TSVT-TVAVRYVGATTASI-SHV-LLVGA-TM--AL-V--v--AVFLV
87 HK10 LEWRNVSGL-VL----p-S-IVYEADDVIL-T---V--VQDGNTST--TSVT-TVAVRYVGATTASI-SHV-LLVGA-TM--AL-V--M--AVFLV
88 S2 LEWRNTSGL-VL----S-S-IVYEADDVIL-T---V--VQDGNTST--TPVT-TVAVRYVGATTASI-SHV-LLVGA-TM--AL-V--M--AVFLV
90 S54 LEWRNTSGL-iL----S-S-IVYEADDVIL-T---V--VQDGNTST--TPVT-TVAVRYVGATTASI-SHV-LLVGA-TL--AL-V--M--AVFLV
89 S52 LEWRNTSGL-vL----S-S-IVYEADDVIL-T---V--VQDGNTSm--TPVT-TVAVRYVGATTASI-SHV-LLVGA-TL--AL-V--M--AVFLV
II/1b 68 IND8 YEVRNVSGV-HV----S-S-IVYEAADMIM-T---V--VREGNfSs--VALT-TLAARNASVpTTTI-rHV-LLVGA-AF--AM-V--L--SVFLV
67 IND5 YEVRNVSGV-HV----S-S-IVYEAADMIM-T---V--VREGNSSR--VALT-TLAARNASVaTTTI-hHV-LLVGA-AF--AM-V--L--SVFLV
73 SW2 YEVRNVSGV-HV----S-S-IVYETADMIM-T---V--VREaNSSR--VALT-TLAARNtSVPTTTI-RHV-LLVGA-AF--vM-V--L--SVFLV
63 HK3 YEVRNVSGI-HV----S-S-vVYETADMIM-T---V--VRENNSSR--VALT-TLAARNVSVPTTTI-RHV-LLVGA-AF--AM-V--L--SVFLV
66 HK8 YEVRNVSGI-HV----S-S-IVYETADMIM-T---m--VRENNSSR--VALT-TLAARNVSVPTTTI-RHV-LLVGA-AF--AM-V--L--SVFLV
71 S45 YEVRNVSGa-HV----S-S-IVYEavDvIl-T---V--VRENNSSR--VALT-TLAARNSSVPTTTI-RHV-LLVGA-AF--AM-V--L--SVFLV
61 D3 YEVRNVSGV-qV----S-S-IVYETADMIM-T---V--VREdNSSR--VALT-TLAARNSSVPTTTI-RHV-LLVGA-AF--AM-V--L--SVFLV
74 T3 YEVRNVSGV-yV----S-S-IVYETADMIM-T---V--VREaNSSR--VALT-TLAARNASVPTkTI-RHV-LLVGA-AF--AM-V--L--SVFLV
65 HK5 YEVRNVSGV-HV----S-l-IVYETtDMIM-T---V--VRENNSSR--VALa-TLAARNASVPTTaI-RHV-LLVGA-AF--AM-V--L--SVFLV
64 HK4 hEVhNVSGI-HV----S-S-IVYEAADMIM-T---V--VRENNSSR--VALT-TLAARNASiPTTTI-RHV-LLVGA-AF--AM-V--L--SVFLV
76 US6 YEVRNVSGm-HV----S-S-IVYEAADMIM-T---V--VRENNSSR--VALT-TLAARNASVPTTTI-RHV-LLVGA-tF--AM-V--L--SVFLI
69 P10 YEVRNVSGv-HV----S-S-IVYEAADMIM-T---V--VRENNSSR--VALT-TLAARNSSVPTTaI-RHV-LLVGA-AF--AM-V--L--SVlLV
72 SA10 YEVRNVSGM-HV----S-S-IVYEAADMIM-T---V--VRENNSSR--VALT-TLAARNSSVPTTTI-RHV-LLVGA-AF--AM-V--L--SVFLV
75 T10 YEVRNVSGM-HV----S-S-IVfEAADlIM-T---V--VREgNSSR--VALT-TLAARNtSVPTTTI-RHV-LLVGA-AF--AM-V--L--SVFLV
62 DK1 YEVRNVSGv-HV----S-S-IVYEAvDVIM-T---V--VREnNhSR--VALT-TLAARNASiPTTTI-RHV-LLVGA-AP--AM-V--L--SVFLV
70 S9 YEVRNVSGa-HV----S-S-IVYEAADVIM-T---V--VgEgNSSq--VALT-TLAARNAtVPTTTI-RHV-LLVGA-vF--AM-V--L--SVFLI
60 D1 YEVRNVSGv-HV----S-S-IVYEtADmIM-T---V--VREdNSSR--VALT-TLAARNGnVPTTaI-RHV-LLVGA-aF--AM-V--L--SVFLI
I/1a 52 DK7 YQVRNSTGL-HV----P-S-IVYEAADAIL-T---V--VREGNvSR--VAMT-TVATRDGKLPTaQL-RHI-LLVGS-TL--AL-V--L--SVFLV
59 US11 YQVRNSTGL-HV----P-S-IVYEAADAIL-T---V--VREGNaSR--VAMT-TVATRDGKLPTTQL-RHI-LLVGS-TL--AL-V--L--SVFLV
55 DR4 HQVRNSTGL-HV----P-S-IVYEAADAIL-T---V--VREGNtSR--VAVT-TVATRDGKLPTTQL-RHI-LLVGS-TL--AL-V--L--SVFLV
54 DR1 HQVRNSTGL-HV----P-S-IVYEAADAIL-a---V--VREGNASR--VAVT-TVATRDGKLPTTQL-RHI-LLVGS-TL--AL-V--L--SVFLV
53 DK9 YQVRNSSGL-HV----P-S-IVYEAADAIL-S---V--VREGNASK--VAVA-TVATRDGKLPATQL-RHI-LLVGS-TL--AL-V--L--SVFLV
58 SW1 YQVRNSSGL-HV----P-S-IVYETADAIL-S---V--VREdqApK--VAVA-TVATRDGKLPATQL-RHI-LLVGS-TL--AL-V--L--SVFLV
56 S14 YQVRNSTGL-HV----P-S-IVYETADAIL-a---V--VREGNtSR--VAmt-TVATRDGKLPATQL-RyI-LLVGS-TL--AL-V--L--SVFLV
57 S18 YQVRNSTGL-HV----P-S-IVYETADtIL-s---V--VREGNaSR--VPVa-TVATRDGKLPATQL-RHI-LLVGS-TL--AL-V--L--SVFLV
4a 91 Z4 ehYRNASGi-Hi----P-S-IVYEAdHhIL-L---V--VmtGNtSR--tPVT-TVAVahpGAPLeSf-RHV-LMVGA-TL--AL-V--L--GAFLm
4c 93 Z6 VNYRNASGV-Hv----P-S-IVYEAEHqIL-L---l--VRvGNQSR--VALT-TVAVsYIGAPLdSl-RHV-LMVGA-TV--AL-V--L--GAFLV
94 Z7 VNYhNASGV-Hi----P-S-ImYEAEHHIL-L---V--VREGNQSR--VALT-TVAApYIGAPLESi-RHV-LMVGA-TV--AL-I--L--GVFLV
4d 95 DK13 yNYRNsSGV-HV----P-S-IVYETdyHIL-L---V--VREGNkSt--VsLT-TVAAghlNAPLESl-RHV-LMVGq-Tl--AL-I--v--GVFLV
4b 92 Z1 VhYRNASGV-HV----P-t-IVYETehHIm-L---V--VRteNtSR--VpLT-TVAAPvpNAPLESm-RHV-LMVGa-Tm--Af-I--l--GVFLV
5a 98 SA5 VPYRNASGV-HV----P-S-IVYEADNLIL-A---V--VkegNVSR--VQIT-TLSAPNLGAVTAPL-RvV-YLAGG-AL--AL-V--A--AVFLV
100 SA7 VPYRNASGV-HV----P-S-IVYEADNLIL-A---V--VRQnNVSR--VQIT-TLSAPNLGAVTAPL-RAV-YLAGG-AL--AL-V--A--AVFLV
97 SA4 VPYRNASGV-HV----P-S-IVYEADNLIL-A---V--VRQDNVSk--VQIT-TLSAPNLGAVTAPL-RAV-YLAGG-AL--AL-V--A--AVFLV
96 SA1 VPYRNASGV-HV----P-S-IVYEADsLIL-A---V--VRQDNVSR--VQIT-TLSAPtfGAVTAPL-RAV-YLAGG-AL--AL-V--A--AVFLV
99 SA6 VPYRNASGV-HV----P-S-IVYEADDLIL-A---V--VRkDNVSR--VhIT-TLSAPSLGAVTAPL-RAV-YLAGG-AL--AL-V--v--AlFLV
101 SA13 VPYRNASGV-HV----P-S-IVYEADDLIL-A---V--VRqgNVSR--VqIT-TLSAPSLGAVTAPL-RAV-YLAGG-AL--AL-V--a--AvFLV
6a 102 HK2 ltYgNsSGl-Hl----P-S-IVlEADamIL-l---l--VRvddrSt--havT-TLalPnastpatgf-RhV-lLAGa-vv--sL-l--l--slFLa

FIGURE 3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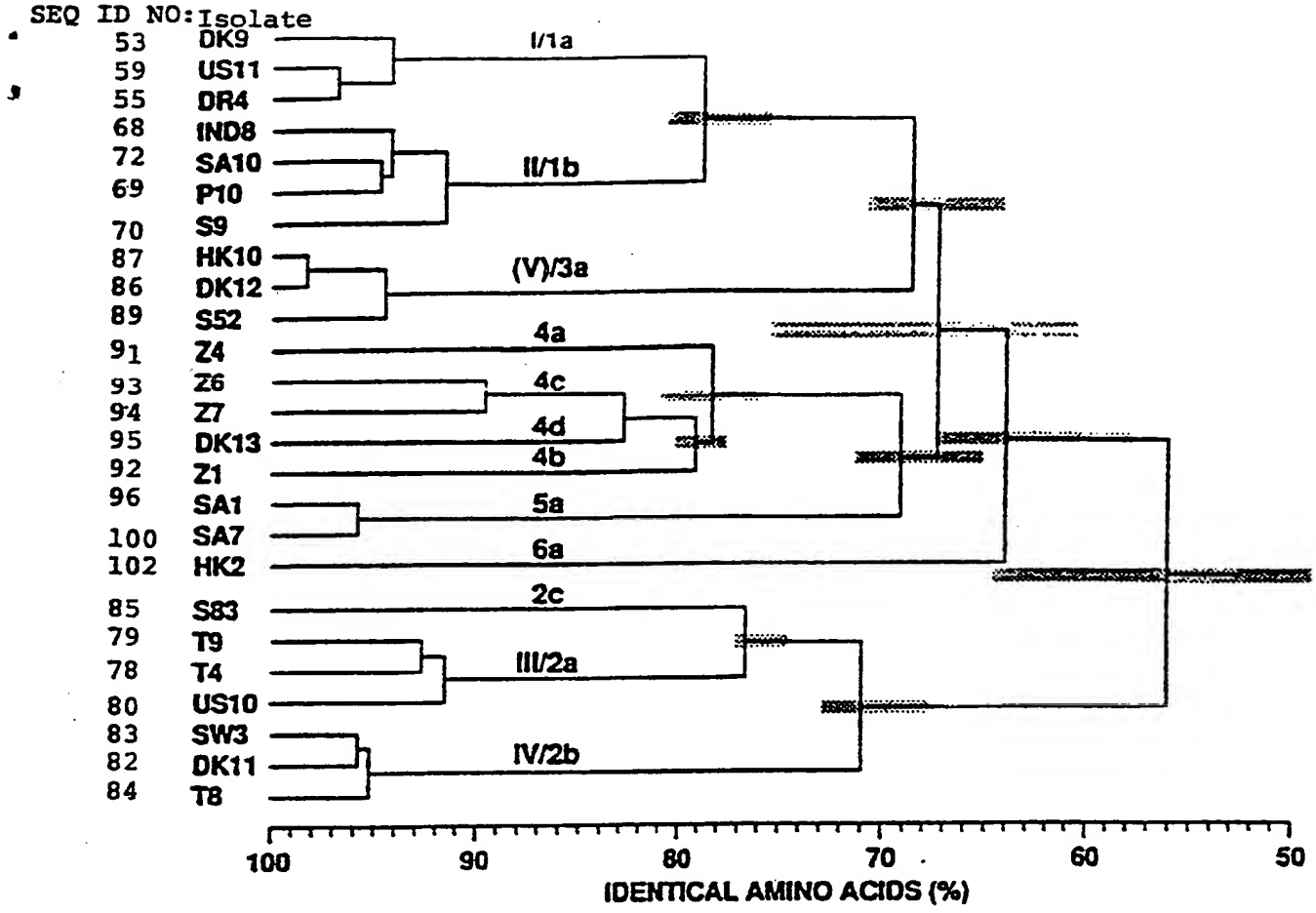
IV/2b
2c
III/2a
(V)/3a
II/1b
I/1a
4a
4c
4d
4b
5a
6a

FIGURE 4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70 S9
87 HK10
86 DK12
89 S52
91 Z4
93 Z6
94 Z7
95 DK13
92 Z1
96 SA1
100 SA7
102 HK2
85 S83
79 T9
78 T4
80 US10
83 SW3
82 DK11
84 T8
I/1a
II/1b
(V)/3a
4a
4c
4d
4b
5a
6a
2c
III/2a
IV/2b
100
90
80
70
60
50
IDENTICAL AMINO ACIDS (%)

FIGURE 5